

GenCore version 5.1.9  
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OM protein - protein search, using SW model

Run on: August 14, 2006, 21:51:58 ; Search time 49 Seconds  
(without alignments)  
239.369 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 1 MCGQDRHMRRLDIDVDQ.....LLQRMHQLSRTGSEDS 134

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: Issued Patents AA.\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/1aa/5 COMB.pdp.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/1aa/6 COMB.pdp.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/1aa/7 COMB.pdp.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/1aa/8 COMB.pdp.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/1aa/9 COMB.pdp.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/1aa/10 COMB.pdp.\*
- 7: /EMC\_Celerra\_SIDS3/prodata/2/1aa/backfill1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	706	99.3	162	2	US-09-522-217-2
2	706	99.3	162	2	US-09-923-246-2
3	706	99.3	162	2	US-10-295-723-2
4	706	99.3	162	2	US-08-825-561A-10
5	706	99.3	162	2	US-10-282-622-2
6	706	99.3	174	2	US-09-949-016-10307
7	695	97.7	519	2	US-09-522-217-85
8	695	97.7	519	2	US-09-923-246-85
9	695	97.7	519	2	US-10-295-723-85
10	694	97.6	162	2	US-10-282-622-6
11	621	87.3	147	2	US-10-282-622-4
12	404	56.8	146	2	US-09-522-217-56
13	404	56.8	146	2	US-09-923-246-56
14	404	56.8	146	2	US-10-295-723-56
15	404	56.8	146	2	US-08-825-561A-47
16	394	55.4	510	2	US-09-522-217-89
17	394	55.4	510	2	US-09-923-246-89
18	394	55.4	510	2	US-10-295-723-89
19	212	29.8	40	2	US-09-522-217-72
20	212	29.8	40	2	US-09-923-246-72
21	212	29.8	40	2	US-10-295-723-72
22	176	24.8	32	2	US-08-522-217-73
23	176	24.8	32	2	US-09-923-246-73
24	176	24.8	32	2	US-10-295-723-73
25	99.5	14.0	114	1	US-08-031-399-6
26	99.5	14.0	114	1	US-08-031-399-12

27	99.5	14.0	114	1	US-08-393-305-3	Sequence 3, Appl1
28	99.5	14.0	114	1	US-08-726-817-3	Sequence 3, Appl1
29	99.5	14.0	114	1	US-08-504-042-6	Sequence 6, Appl1
30	99.5	14.0	114	1	US-08-504-042-12	Sequence 12, Appl1
31	99.5	14.0	114	1	US-08-725-969-3	Sequence 3, Appl1
32	99.5	14.0	114	1	US-08-794-524-3	Sequence 3, Appl1
33	99.5	14.0	114	2	US-09-189-193-3	Sequence 20, Appl1
34	99.5	14.0	114	2	US-09-462-941-40	Sequence 6, Appl1
35	99.5	14.0	114	5	PCT-US94-03793-6	Sequence 6, Appl1
36	99.5	14.0	114	5	PCT-US94-03793-12	Sequence 12, Appl1
37	99.5	14.0	162	1	US-08-031-399-5	Sequence 5, Appl1
38	99.5	14.0	162	1	US-08-393-305-2	Sequence 2, Appl1
39	99.5	14.0	162	1	US-08-535-733-2	Sequence 2, Appl1
40	99.5	14.0	162	1	US-08-726-817-2	Sequence 2, Appl1
41	99.5	14.0	162	1	US-08-504-042-5	Sequence 2, Appl1
42	99.5	14.0	162	1	US-08-725-969-2	Sequence 2, Appl1
43	99.5	14.0	162	1	US-08-794-524-2	Sequence 2, Appl1
44	99.5	14.0	162	1	US-08-842-947-6	Sequence 6, Appl1
45	99.5	14.0	162	2	US-09-189-193-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-09-522-217-2  
Sequence 2, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:  
APPLICANT: No. 6307024aK, Julia E.

APPLICANT: Preenell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Grose, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Tracey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER APPLICATION NUMBER: US 60/142,013

EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 162

TYPE: PRT

ORGANISM: Homo sapiens

US-09-522-217-2

Query Match

Best Local Similarity 100.0%; Pred. No. 5.4e-73;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGQDRHMRRLDIDVDQKYNVDLPFLPAPDEVNTGCSAASCPKAKLKANT 61

Db 30 QGQDRHMRRLDIDVDQKYNVDLPFLPAPDEVNTGCSAASCPKAKLKANT 89

QY 62 GNNRIINVSIIKKLKRKPETNAGROKRLTSCSYEKPKPEFLERFKSLIQMIIH 121

Db 90 GNNRIINVSIIKKLKRKPETNAGROKRLTSCSYEKPKPEFLERFKSLIQMIIH 149

QY 122 QHLSRTGSEDS 134

Db 150 QHLSRTGSEDS 162

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2006, 21:51:58 ; Search time 49 Seconds

(without alignments)  
239.369 Million cell updates/sec

Title: US-10-735-149-28

Sequence: 1 MCGGDRHMRQLDIDVDQ.....LLQGMHQLSSRTGSEDS 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/5.COMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/6.COMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/7.COMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/H.COMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/RE.COMB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	706	99.3	162	2	US-09-522-217-2 Sequence 2, Appli
2	706	99.3	162	2	US-09-923-246-2 Sequence 2, Appli
3	706	99.3	162	2	US-10-295-723-2 Sequence 2, Appli
4	706	99.3	162	2	US-09-825-561A-10 Sequence 10, Appli
5	706	99.3	162	2	US-10-282-622-2 Sequence 2, Appli
6	706	99.3	174	2	US-09-949-016-10307 Sequence 10307, A
7	695	97.7	519	2	US-09-522-217-85 Sequence 85, Appli
8	695	97.7	519	2	US-09-923-246-85 Sequence 85, Appli
9	695	97.7	519	2	US-10-295-723-85 Sequence 85, Appli
10	694	97.6	162	2	US-10-282-622-6 Sequence 6, Appli
11	621	87.3	147	2	US-10-282-622-4 Sequence 4, Appli
12	404	56.8	146	2	US-09-522-217-56 Sequence 56, Appli
13	404	56.8	146	2	US-09-923-246-56 Sequence 56, Appli
14	404	56.8	146	2	US-10-295-723-56 Sequence 56, Appli
15	404	56.8	146	2	US-09-825-561A-47 Sequence 47, Appli
16	394	55.4	510	2	US-09-522-217-89 Sequence 89, Appli
17	394	55.4	510	2	US-09-923-246-89 Sequence 89, Appli
18	394	55.4	510	2	US-10-295-723-89 Sequence 89, Appli
19	212	29.8	40	2	US-09-522-217-72 Sequence 72, Appli
20	212	29.8	40	2	US-09-923-246-72 Sequence 72, Appli
21	212	29.8	40	2	US-10-295-723-72 Sequence 72, Appli
22	176	24.8	32	2	US-09-522-217-73 Sequence 73, Appli
23	176	24.8	32	2	US-09-923-246-73 Sequence 73, Appli
24	176	24.8	32	2	US-10-295-723-73 Sequence 73, Appli
25	99.5	14.0	114	1	US-08-031-399-6 Sequence 6, Appli
26	99.5	14.0	114	1	US-08-031-399-12 Sequence 12, Appli

27	99.5	14.0	114	1	US-08-393-305-3 Sequence 3, Appli
28	99.5	14.0	114	1	US-08-726-817-3 Sequence 3, Appli
29	99.5	14.0	114	1	US-08-504-042-6 Sequence 6, Appli
30	99.5	14.0	114	1	US-08-504-042-12 Sequence 12, Appli
31	99.5	14.0	114	1	US-08-725-969-3 Sequence 3, Appli
32	99.5	14.0	114	1	US-08-794-524-3 Sequence 3, Appli
33	99.5	14.0	114	2	US-09-189-193-3 Sequence 3, Appli
34	99.5	14.0	114	2	US-09-462-941-20 Sequence 20, Appli
35	99.5	14.0	114	5	PCT-US94-03793-6 Sequence 6, Appli
36	99.5	14.0	114	5	PCT-US94-03793-12 Sequence 12, Appli
37	99.5	14.0	162	1	US-08-031-399-5 Sequence 5, Appli
38	99.5	14.0	162	1	US-08-393-305-2 Sequence 2, Appli
39	99.5	14.0	162	1	US-08-535-733-2 Sequence 2, Appli
40	99.5	14.0	162	1	US-08-726-817-2 Sequence 2, Appli
41	99.5	14.0	162	1	US-08-504-042-5 Sequence 5, Appli
42	99.5	14.0	162	1	US-08-725-969-2 Sequence 2, Appli
43	99.5	14.0	162	1	US-08-794-524-2 Sequence 2, Appli
44	99.5	14.0	162	2	US-08-842-947-6 Sequence 6, Appli
45	99.5	14.0	162	2	US-09-189-193-2 Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-09-522-217-2  
Sequence 2, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:  
APPLICANT: No. 6307024ak, Julia E.

APPLICANT: Preenell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey K.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123,547

EARLIER FILING DATE: 1999-03-09

EARLIER FILING DATE: 1999-03-09

EARLIER FILING DATE: 1999-03-09

EARLIER FILING DATE: 1999-03-09

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EARLIER FILING DATE: 1999-03-09

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RESULT 2
US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. 6605272
; GENERAL INFORMATION:
; APPLICANT: No. 6605272ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-2

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Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      30  QGQDRHMIRKQRLIDIVDQKNYVNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 89
Qy      62  GNNERRIINVSIKKLKRRPSTNAGRQKHRLTCPSCDSEYKKPKPEFLERFKSLLOQMIIH 121
Db      90  GNNERRIINVSIKKLKRRPSTNAGRQKHRLTCPSCDSEYKKPKPEFLERFKSLLOQMIIH 149
Qy      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162

RESULT 3
US-10-295-723-2
; Sequence 2, Application US/10295723
; Patent No. 6686178
; GENERAL INFORMATION:
; APPLICANT: No. 6686178ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
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; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-2

Query Match          99.3%; Score 706; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  QGQDRHMIRKQRLIDIVDQKNYVNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 61
Db      30  QGQDRHMIRKQRLIDIVDQKNYVNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 89
Qy      62  GNNERRIINVSIKKLKRRPSTNAGRQKHRLTCPSCDSEYKKPKPEFLERFKSLLOQMIIH 121
Db      90  GNNERRIINVSIKKLKRRPSTNAGRQKHRLTCPSCDSEYKKPKPEFLERFKSLLOQMIIH 149
Qy      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162

RESULT 4
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. 677539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-561A-10

Query Match          99.3%; Score 706; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 5.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  QGQDRHMIRKQRLIDIVDQKNYVNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 61
Db      30  QGQDRHMIRKQRLIDIVDQKNYVNDLVPEFLPAPEDEVETNCESAFSCFOKQOLKSANT 89
Qy      62  GNNERRIINVSIKKLKRRPSTNAGRQKHRLTCPSCDSEYKKPKPEFLERFKSLLOQMIIH 121
Db      90  GNNERRIINVSIKKLKRRPSTNAGRQKHRLTCPSCDSEYKKPKPEFLERFKSLLOQMIIH 149
Qy      122 QHLSRTHGSEDS 134
Db      150 QHLSRTHGSEDS 162
```

;  
; APPLICANT: Sprecher, Cindy A.  
;  
; APPLICANT: Foster, Donald C.  
;  
; APPLICANT: Holly, Richard D.  
;  
; APPLICANT: Gross, Jane A.  
;  
; APPLICANT: Johnston, Janet V.

```
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 519
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MBP-human zalphal1 ligand fusion polypeptide
US-09-923-246-85
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Query Match          97.7%; Score 695; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      389 ODRHMIRMRQLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANTGN 448
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Db      449 NERIINVSICKLKKRPSTNAGRQKRLTGPCSDSYEKKPKEFLERFKSLLOKMIHOH 508
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Qy      124 LSSRTHGSEDS 134
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Db      509 LSSRTHGSEDS 519
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RESULT 9
US-10-295-723-85
Sequence 85, Application US/10295723
Patent No. 6686178
GENERAL INFORMATION:
APPLICANT: No. 6686178a, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 85
LENGTH: 519
TYPE: PRT
ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: MBP-human zalphal1 ligand fusion polypeptide
US-10-295-723-85
Query Match          97.7%; Score 695; DB 2; Length 519;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      4 ODRHMIRMRQLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANTGN 63
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Db      389 ODRHMIRMRQLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANTGN 448
      |||
Qy      64 NERIINVSICKLKKRPSTNAGRQKRLTGPCSDSYEKKPKEFLERFKSLLOKMIHOH 123
      |||
Db      449 NERIINVSICKLKKRPSTNAGRQKRLTGPCSDSYEKKPKEFLERFKSLLOKMIHOH 508
      |||
Qy      124 LSSRTHGSEDS 134
      |||
Db      509 LSSRTHGSEDS 519
```

```
RESULT 10
US-10-282-622-6
Sequence 6, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932a, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/337,586
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 162
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: zalphal1 ligand Q153D/I156D
US-10-282-622-6
```

```
Query Match          97.6%; Score 694; DB 2; Length 162;
Best Local Similarity 98.5%; Pred. No. 1.3e-71;
Matches 131; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      2 OGDHRMIRMRQLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANT 61
      |||
Db      30 OGDHRMIRMRQLIDIVDQKNVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANT 89
      |||
Qy      62 GNERIINVSICKLKKRPSTNAGRQKRLTGPCSDSYEKKPKEFLERFKSLLOKMIH 121
      |||
Db      90 GNERIINVSICKLKKRPSTNAGRQKRLTGPCSDSYEKKPKEFLERFKSLLOKMIH 149
      |||
Qy      122 QHLSRTHGSEDS 134
      |||
Db      150 QHLSRTHGSEDS 162
```

```
RESULT 11
US-10-282-622-4
Sequence 4, Application US/10282622
Patent No. 6929932
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. 6929932a, Julia E.
TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
```

PRIOR APPLICATION NUMBER: 09/522,217

```

1 PRIOR FILING DATE: 2000-03-09
2 PRIOR APPLICATION NUMBER: US 60/123,547
3 PRIOR FILING DATE: 1999-03-09
4 PRIOR APPLICATION NUMBER: US 60/123,904
5 PRIOR FILING DATE: 1999-03-11
6 PRIOR APPLICATION NUMBER: US 60/142,013
7 PRIOR FILING DATE: 1999-07-01
8 NUMBER OF SEQ ID NOS: 115
9 SOFTWARE: FastSeq for Windows Version 3.0
10 SEQ ID NO 56
11 LENGTH: 146
12 TYPE: prt
13 ORGANISM: mus musculus
14 OS-10-295-723-56

```

Query Match	56.8%;	Score 404;	DB 2;	Length 146;
Best Local Similarity	62.1%;	Pred. No. 2e-38;		
Matches 77;	Conservative 19;	Mismatches 28;	Indels 0;	Gaps 0;

```

Qy  2  QCGDRMIRNRQIJDIDVDLQKTVYVDVVEEFLPAEDVETCEMSAFSCFQKALCKSANT 61
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db  23  QCGDRLLIRLRHIDIVEQIKTIYENDLDPBELLASQDVKGCEHAAFACFQKALCKSPNP 82
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Qy  62  GNNERLIINSIKKLRKPPSTNAGROKRRHLCPSCDSEYKKPPEFLERPKSLIQMTH 121
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db  83  GNNKTFILIDVAQRLRRRLPARRGKKQKHIAKPCSDSEYKTFPEFLERKMLQJOMTH 142
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Qy  122 QHLS 125
      |||
Db  143 QHLS 146
      |||

```

```

RESULT 15
US-09-825-561A-47
Sequence 47, Application US/09825561A
Patent No. 6777539
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 6777539ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Presnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPAA1 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 146
TYPE: PR1
ORGANISM: Mus musculus
US-09-825-561A-47

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Query Match 56.8%; Score 404; DB 2; Length 146;  
Best Local Similarity 62.1%; Pred. No. 2e-38;  
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

```

Qy      2  QGODRHMIRNRRLDIPVDLKNVNDLVBEFLPADEVDETCEMSAFSCFOKALUJSTAN 61
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      23  QGSDRLIRLRRLHLDIVBOLKIYENDLDBELLISAFQVKGHCENAFACFOKALKFSNP 82
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy      62  GNNERLIINVSIKKLAKRPPSTNAGROROKRLTLPSCDSYERKKPPEFLERFSLLOMIH 121
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      83  GNNKTFILIDVQLRRRLPARGGKKQKRIACPSCDSEYERKTPREFLERLKWLLQGMTH 142
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy      122  QHLS 125
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

Db 143 QHLS 146

Search completed: August 14, 2006, 21:53:20  
Job time : 49 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: August 14, 2006, 21:52:43 ; Search time 180 Seconds  
(without alignments)  
344.838 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711

Sequence: 1 MCGDRHMRIRQLIDIVDQ.....LLQRMHQLHSRTGSEDS 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_Main.\*  
1: /EMC\_Ceiera\_SIDS3/ptocdata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Ceiera\_SIDS3/ptocdata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Ceiera\_SIDS3/ptocdata/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Ceiera\_SIDS3/ptocdata/2/pubppaa/US10\_PUBCOMB.pep:\*  
5: /EMC\_Ceiera\_SIDS3/ptocdata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Ceiera\_SIDS3/ptocdata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	706	99.3	133	5	US-10-867-992-19
2	706	99.3	162	3	US-09-923-246-2
3	706	99.3	162	3	US-09-825-561A-10
4	706	99.3	162	3	US-09-972-218A-19
5	706	99.3	162	4	US-10-264-634-19
6	706	99.3	162	4	US-10-295-723-2
7	706	99.3	162	4	US-10-282-622-2
8	706	99.3	162	4	US-10-456-780-2
9	706	99.3	162	4	US-10-659-684-2
10	706	99.3	162	4	US-10-620-169-2
11	706	99.3	162	5	US-10-872-087-10
12	706	99.3	162	5	US-10-787-442-2
13	706	99.3	162	5	US-10-951-239-2
14	706	99.3	162	5	US-10-775-204-2177
15	706	99.3	162	6	US-11-174-398-2
16	706	99.3	162	6	US-11-134-489-2
17	706	99.3	162	6	US-11-132-987-5
18	706	99.3	162	6	US-11-197-468-19
19	706	99.3	162	6	US-10-775-204-2167
20	696	97.9	160	6	US-11-197-221-1
21	695	97.7	131	5	US-10-867-992-16
22	695	97.7	131	6	US-11-132-947-2
23	695	97.7	519	3	US-09-923-246-85
24	695	97.7	519	4	US-10-295-723-85
25	695	97.7	519	4	US-10-659-684-85
26	695	97.7	519	5	US-10-787-442-85
27	694	97.6	162	4	US-10-282-622-6

28	694	97.6	162	6	US-11-174-398-6	Sequence 6, Appli
29	661	93.0	133	5	US-10-867-992-12	Sequence 12, Appli
30	656	92.3	133	5	US-10-867-992-14	Sequence 14, Appli
31	650	91.4	131	5	US-10-867-992-10	Sequence 10, Appli
32	645	90.7	131	5	US-10-867-992-4	Sequence 4, Appli
33	645	90.7	131	5	US-10-867-992-6	Sequence 6, Appli
34	644	90.6	131	5	US-10-867-992-8	Sequence 8, Appli
35	642	90.3	131	5	US-10-867-992-2	Sequence 2, Appli
36	621	87.3	147	4	US-10-282-622-4	Sequence 4, Appli
37	621	87.3	147	6	US-11-174-398-4	Sequence 4, Appli
38	535	75.2	152	6	US-11-132-947-12	Sequence 12, Appli
39	404	56.8	146	3	US-09-923-246-56	Sequence 56, Appli
40	404	56.8	146	3	US-09-825-561A-47	Sequence 47, Appli
41	404	56.8	146	4	US-10-295-723-56	Sequence 56, Appli
42	404	56.8	146	4	US-10-456-780-4	Sequence 4, Appli
43	404	56.8	146	4	US-10-659-684-56	Sequence 56, Appli
44	404	56.8	146	5	US-10-872-087-47	Sequence 47, Appli
45	404	56.8	146	5	US-10-787-442-56	Sequence 56, Appli

## ALIGNMENTS

```

RESULT 1
US-10-867-992-19
; Sequence 19, Application US/10867992
; Publication No. US20050124044A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark R.; Heavner, George A.; Luo, Jinqian; Song, Xiao-yu R.
; TITLE OF INVENTION: Interleukin-21 Analogs
; FILE REFERENCE: CEN5029 NP
; CURRENT APPLICATION NUMBER: US/10/867,992
; CURRENT FILING DATE: 2004-06-15
; PRIOR APPLICATION NUMBER: US 60/427,772
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 19
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-867-992-19

Query Match      99.3%; Score 706; DB 5; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2  QGDRHMRIRQLIDIVDQLNKYNVDLVPFRLPAPBDVETNCWSAFSCFOKAQKSNANT 61
      |||
Db      1  QGDRHMRIRQLIDIVDQLNKYNVDLVPFRLPAPBDVETNCWSAFSCFOKAQKSNANT 60

Cy      62  GNNRIINVSITKIKRRKPPSTNAGRGRKHRLTCPCSCSYEKKPKPEFLERKSLQKMIH 121
      |||
Db      61  GNNRIINVSITKIKRRKPPSTNAGRGRKHRLTCPCSCSYEKKPKPEFLERKSLQKMIH 120

Cy      122  QHLSRTHGSEDS 134
      |||
Db      121  QHLSRTHGSEDS 133

RESULT 2
US-09-923-246-2
; Sequence 2, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.

```

```

1  APPLICANT: Dillon, Stacey R.
2  APPLICANT: Hammond, Angela K.
3  TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
4  FILE REFERENCE: 99-16
5  CURRENT APPLICATION NUMBER: US/09/923.246
6  PRIOR FILING DATE: 2001-08-03
7  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522.217
8  PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
9  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
10 PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
11 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
12 PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
13 NUMBER OF SEQ ID NOS: 115
14 SOFTWARE: FastSeq for Windows Version 3.0
15 SEQ ID NO 2
16 LENGTH: 162
17 TYPE: prt
18 ORGANISM: Homo sapiens
19 US-09-923-246-2

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Query Match	99.3%;	Score 706;	DB 3;	Length 162;
Best Local Similarity	100.0%;	Pred. NO. 4.7e-67;		
Matches 133; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2	QCGDRMIMRQOLIDIVDQKKNYVNDVLEFELPAPDEVETNCMSAFSCFQKALKEANT	61
Db	30	QCGDRMIMRQOLIDIVDQKKNYVNDVLEFELPAPDEVETNCMSAFSCFQKALKEANT	89
QY	62	GNNRRILINSLIKKLRKPRSTNAGRRQKRLTLCSCDSYKKKKPREFLERKSLLOMTH	121
Db	90	GNNRRILINSLIKKLRKPRSTNAGRRQKRLTLCSCDSYKKKKPREFLERKSLLOMTH	149
QY	122	QHLSTRHGSDEDS	134
Db	150	QHLSTRHGSDEDS	162

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RESULT 3
US-09-825-561A-10
; Sequence 10, Application US/09825561A
; Patent No. US20020137677A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. US20020137677A1ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPAA1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: prt
; ORGANISM: Homo sapiens
; IS-09-825-561A-10

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Query Match 99.3%; Score 706; DB 3; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Gaps 0;

QY	2	QCGDRHMTMRQLDIIVDQKKNYVNDVPEELPAEDVETNCMSAFSCFOKAQJSAANT	61
Db	30	QCGDRHMTMRQLDIIVDQKKNYVNDVPEELPAEDVETNCMSAFSCFOKAQJSAANT	89
QY	62	GNNERTINVISIKKLRRKPPSTNAGRRQHRLLTCSCDSYEKKKPEKLEPRKSLIQMIIH	121

Db 90 GNNERILINISIKLKRPPSTNAGRQKRLTCSQSYKKQPEKPELEPKSLQRMTH 149

Qy 122 QHLSRRTGSEDS 134

Db 150 QHLSRRTGSEDS 162

US-09-972-218A-19  
; Sequence 19, Application US/09972218A  
; Publication No. US20030049798A1

```

APPLICANT: Carter, Laura
APPLICANT: Whitters, Matthew J
APPLICANT: Collins, Mary
APPLICANT: Young, Deborah A.
APPLICANT: Donaldson, Debra D.
APPLICANT: Lowe, Leslie D.
APPLICANT: Unger, Michelle
TITLE OF INVENTION: MO-1, Member of the Cytokine Receptor Family
FILE REFERENCE: 22058-552CIP2
CURRENT APPLICATION NUMBER: US/09/972,218A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/569384
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 09/560766
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US/6057128
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 162
TYPE: PRT
ORGANISM: Human
IS-09-972-218A-19

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Query Match	99.3%;	Score 706;	DB 3;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 4.7e-67;		
Matches 133;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	2	QGQDRHMRRLIDIVDQKKNVNDLVPEFLPAPEDVETNCWSAFSCFOKAQKLSANT	61	
Db	30	QGQDRHMRRLIDIVDQKKNVNDLVPEFLPAPEDVETNCWSAFSCFOKAQKLSANT	89	
QY	62	GNNERIINVSIIKKIKRRPSTNAGRQKHRLTCPSCSYEEKKPKFLERFKSLQKMIH	121	
Db	90	GNNERIINVSIIKKIKRRPSTNAGRQKHRLTCPSCSYEEKKPKFLERFKSLQKMIH	149	
QY	122	QHLSSRTHGSEDS	134	
Db	150	QHLSSRTHGSEDS	162	

```

RESULT 5
US-10-264-634-19
: Sequence 19, Application US/10264634
: Publication No. US20030108549A1
: GENERAL INFORMATION:
: APPLICANT: Donaldson, Debra et al.
: TITLE OF INVENTION: Methods and Compositions for Modulating Interleukin-21 Receptor Ac
: FILE REFERENCE: G15320-P3
: CURRENT APPLICATION NUMBER: US/10/264,634
: PRIOR FILING DATE: 2002-10-04
: PRIOR APPLICATION NUMBER: 09/040,005
: PRIOR FILING DATE: 1998-03-17
: PRIOR APPLICATION NUMBER: 09/560,766
: PRIOR FILING DATE: 2000-04-26
: PRIOR APPLICATION NUMBER: 09/569,384
: PRIOR FILING DATE: 2000-05-11
: PRIOR APPLICATION NUMBER: 09/972,218
: PRIOR FILING DATE: 2001-10-04

```

```

1  SER ID NO 19
2  LENGTH: 162
3  TYPE: PRT
4  ORGANISM: Human
5  OS-10-264-634-19

```

Query Match	99.3%	Score 706;	DB 4;	Length 162;
Best Local Similarity	100.0%	Pred. No. 4.7e-67;		
Matches 133; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	2	QGGDRHMIRKQLIDVDLKNYVNLVEFPAPEDEVTCNMFAPFCFOKAOLKSANT	61
Db	30	QGGDRHMIRKQLIDVDLKNYVNLVEFPAPEDEVTCNMFAPFCFOKAOLKSANT	89
Qy	62	GNNERIINYSIKLKKRPSTNAGRQKRLTCPSCDSEYKKPKFLEFRKSLLOKMIH	121
Db	90	GNNERIINYSIKLKKRPSTNAGRQKRLTCPSCDSEYKKPKFLEFRKSLLOKMIH	149
Qy	122	QHLSSRTGSEDS	134
Db	150	QHLSSRTGSEDS	162

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RESULT 6
US-10-295-723-2
Sequence 2, Application US/10295723
Publication NO. US20030125524A1
GENERAL INFORMATION:
  APPLICANT: No. US20030125524A1ak, Julia E.
  APPLICANT: Plesnell, Scott R.
  APPLICANT: Sprecher, Cindy A.
  APPLICANT: Foster, Donald C.
  APPLICANT: Holly, Richard D.
  APPLICANT: Gross, Jane A.
  APPLICANT: Johnston, Janet V.
  APPLICANT: Nelson, Andrew J.
  APPLICANT: Dillon, Stacy R.
  APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/10/295,723
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: 09/522,217
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/123,547
PRIOR FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: US 60/123,904
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 60/142,013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-723-2

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Query Match	99.3%	Score	706	DB	4	Length	162
Best Local Similarity	100.0%	Pred. No.	4,76-67				
Matches	133	Conservative	0	Mismatches	0	Indels	0
QY	2	QGQGRHMTBMSQGLDIDYDQKKNVYVDVPEPLPAEDVETNCEMAFSCFOAKQKLSANT	61				
DB	30	QGQGRHMTBMSQGLDIDYDQKKNVYVDVPEPLPAEDVETNCEMAFSCFOAKQKLSANT	89				
QY	62	GNNERIINVASIKGLKKRKPSTNAGRQGRRLTCSPCDSYEKKPPEPLERFSKLLQNMH	121				
DB	90	GNNERIINVASIKGLKKRKPSTNAGRQGRRLTCSPCDSYEKKPPEPLERFSKLLQNMH	149				

QY	122	QHLSSRTHGSEDS	134
Db	150	QHLSSRTHGSEDS	162

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RESULT 7
US-10-282-622-2
Sequence 2, Application US/10282622
Publication NO. US20030134390A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: West, James W.
APPLICANT: No. US20030134390A1ak, Julia B.
TITLE OF INVENTION: ZALPHRA1 LIGAND ANTAGONISTS
FILE REFERENCE: 01-37
CURRENT APPLICATION NUMBER: US/10/282,622
CURRENT FILING DATE: 2002-10-28
PRIORITY APPLICATION NUMBER: 60/337,586
PRIORITY FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 30
SOFTWARE: SeqSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRT
ORGANISM: Homo sapiens
US-10-282-622-2

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Query	2	QGGDRHMI RMQLIDVDLKNVYNDLVEFLPADEVTNCEWSAFSCFOKAQLKSANT	61
Db	30	QGGDRHMI RMQLIDVDLKNVYNDLVEFLPADEVTNCEWSAFSCFOKAQLKSANT	89
Qy	62	GNNRRRIINVSFKKLKRPPSTNAGRRQGRRLTCPCSDSYEKKPPREFLERFSLLOKMT	121
Db	90	GNNRRRIINVSFKKLKRPPSTNAGRRQGRRLTCPCSDSYEKKPPREFLERFSLLOKMT	149
Qy	122	QHLSSRTGSEDS	134
Db	150	QHLSSRTGSEDS	162

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RESULT 8
US-10-456-780-2
Sequence 2, Application US/10456780
Publication No. US20040009150A1
GENERAL INFORMATION:
APPLICANT: Nelson, Andrew J.
APPLICANT: Hughes, Steven D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: US OF IL-21 IN CANCER
TITLE OF INVENTION: OTHER THERAPEUTIC AP
FILE REFERENCE: 03-08
CURRENT APPLICATION NUMBER: US/10/456,780
CURRENT FILING DATE: 2003-06-06
PRIOR APPLICATION NUMBER: US 60/387,127
PRIOR FILING DATE: 2002-06-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 162
TYPE: PRN
ORGANISM: Homo sapiens
US-10-456-780-2

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Query Match	99.3%;	Score 706;	DB 4;	Length 162;
Best Local Similarity	100.0%;	Pred. No. 4.	7e-67;	
Matches 133;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
Oy	2	QGDDRHRIRKQILIDYDQLKNYVNDLVPEFLPAPEDETVCMSAFSCFQKQQLKSANT	61	

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Db      30 QGODRHMRKQLIDIVDQKNYNDLVPEFLPAPBEDVETNCESAFSCFOKQKLSANT 89
      62 GNNERIINVSISKUKRKPSTNAGROKRLTSPSCDSYEKKPKPEFLERFKSLQGMIIH 121
      90 GNNERIINVSISKUKRKPSTNAGROKRLTSPSCDSYEKKPKPEFLERFKSLQGMIIH 149

QY      122 QHLSRTHGSEDS 134
      150 QHLSRTHGSEDS 162

RESULT 9
US-10-659-684-2
; Sequence 2, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-684-2

Query Match      99.3%; Score 706; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QGODRHMRKQLIDIVDQKNYNDLVPEFLPAPBEDVETNCESAFSCFOKQKLSANT 61
      30 QGODRHMRKQLIDIVDQKNYNDLVPEFLPAPBEDVETNCESAFSCFOKQKLSANT 89
      62 GNNERIINVSISKUKRKPSTNAGROKRLTSPSCDSYEKKPKPEFLERFKSLQGMIIH 121
      90 GNNERIINVSISKUKRKPSTNAGROKRLTSPSCDSYEKKPKPEFLERFKSLQGMIIH 149

QY      122 QHLSRTHGSEDS 134
      150 QHLSRTHGSEDS 162

RESULT 10
US-10-620-169-2
; Sequence 2, Application US/10620169
; Publication No. US20040136954A1
; GENERAL INFORMATION:
; APPLICANT: Grusby, Michael J
; APPLICANT: Wurster, Andrea
; APPLICANT: Young, Deborah
; APPLICANT: Collins, Mary
```

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; APPLICANT: Whitters, Matthew
; TITLE OF INVENTION: Methods and Compositions for Modulating T Helper (TH)
; FILE REFERENCE: 23058-585
; CURRENT APPLICATION NUMBER: US/10/620,169
; PRIOR APPLICATION NUMBER: 60/396,160
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/403,001
; PRIOR FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-620-169-2

Query Match      99.3%; Score 706; DB 4; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QGODRHMRKQLIDIVDQKNYNDLVPEFLPAPBEDVETNCESAFSCFOKQKLSANT 61
      30 QGODRHMRKQLIDIVDQKNYNDLVPEFLPAPBEDVETNCESAFSCFOKQKLSANT 89
      62 GNNERIINVSISKUKRKPSTNAGROKRLTSPSCDSYEKKPKPEFLERFKSLQGMIIH 121
      90 GNNERIINVSISKUKRKPSTNAGROKRLTSPSCDSYEKKPKPEFLERFKSLQGMIIH 149

QY      122 QHLSRTHGSEDS 134
      150 QHLSRTHGSEDS 162

RESULT 11
US-10-872-087-10
; Sequence 10, Application US/10872087
; Publication No. US20040235743A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Novak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA1 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22D1
; CURRENT APPLICATION NUMBER: US/10/872,087
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 09/825,561
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-087-10

Query Match      99.3%; Score 706; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 4.7e-67;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QGODRHMRKQLIDIVDQKNYNDLVPEFLPAPBEDVETNCESAFSCFOKQKLSANT 61
      30 QGODRHMRKQLIDIVDQKNYNDLVPEFLPAPBEDVETNCESAFSCFOKQKLSANT 89
      62 GNNERIINVSISKUKRKPSTNAGROKRLTSPSCDSYEKKPKPEFLERFKSLQGMIIH 121
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Db 90 GNNERIINVSIKLKRRPPTNAGRRQKRLTCSGCSYKKPKPEFLERFKSLLOKMIH 149  
QY 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

## RESULT 12

US-10-787-442-2  
Sequence 2, Application US/10787442  
Publication No. US2004026065A1

## GENERAL INFORMATION:

APPLICANT: NOVAK, Julia E.  
APPLICANT: Presnell, Scott R.  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Foster, Donald C.  
APPLICANT: Holly, Richard D.  
APPLICANT: Grobs, Jane A.  
APPLICANT: Johnston, Janet V.  
APPLICANT: Nelson, Andrew J.  
APPLICANT: Dillon, Stacey R.  
APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA1 LIGAND  
FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/10/787,442  
CURRENT FILING DATE: 2004-02-26  
PRIOR APPLICATION NUMBER: US/09/522,217  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: US 60/123,547  
PRIOR FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: US 60/123,904  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: US 60/142,013  
PRIOR FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-787-442-2

Query Match 99.3%; Score 706; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMRKQOLIDIVDLKNTVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 61  
Db 30 QGDRHMRKQOLIDIVDLKNTVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 89  
QY 62 GNNERIINVSIKLKRRPPTNAGRRQKRLTCSGCSYKKPKPEFLERFKSLLOKMIH 121  
Db 90 GNNERIINVSIKLKRRPPTNAGRRQKRLTCSGCSYKKPKPEFLERFKSLLOKMIH 149  
QY 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

## RESULT 13

US-10-951-239-2  
Sequence 2, Application US/10951239  
Publication No. US20050095223A1

## GENERAL INFORMATION:

APPLICANT: Sivakumar, Pallavur  
APPLICANT: Nelson, Andrew  
TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES  
FILE REFERENCE: 03-09  
CURRENT APPLICATION NUMBER: US/10/951,239  
CURRENT FILING DATE: 2004-09-27  
PRIOR APPLICATION NUMBER: 60/505,919  
PRIOR FILING DATE: 2003-09-25

NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-951-239-2

Query Match 99.3%; Score 706; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMRKQOLIDIVDLKNTVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 61  
Db 30 QGDRHMRKQOLIDIVDLKNTVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 89  
QY 62 GNNERIINVSIKLKRRPPTNAGRRQKRLTCSGCSYKKPKPEFLERFKSLLOKMIH 121  
Db 90 GNNERIINVSIKLKRRPPTNAGRRQKRLTCSGCSYKKPKPEFLERFKSLLOKMIH 149  
QY 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

## RESULT 14

US-10-775-204-2177  
Sequence 2177, Application US/10775204  
Publication No. US2005018664A1

## GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.  
APPLICANT: Haseltine, William A.  
APPLICANT: Balance, David J.  
APPLICANT: Turner, Andrew J.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PF564  
CURRENT APPLICATION NUMBER: US/10/775,204  
CURRENT FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/341,811  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/360,000  
PRIOR FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: 60/378,950  
PRIOR FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: 60/398,008  
PRIOR FILING DATE: 2002-07-24  
PRIOR APPLICATION NUMBER: 60/411,355  
PRIOR FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: 60/414,984  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: 60/417,611  
PRIOR FILING DATE: 2002-10-11  
PRIOR APPLICATION NUMBER: 60/420,246  
PRIOR FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: 60/423,623  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/351,360  
PRIOR FILING DATE: 2002-01-28

Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2222  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2177  
LENGTH: 162  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-775-204-2177

Query Match 99.3%; Score 706; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMRKQOLIDIVDLKNTVNDLVPEFLPAPEDVETNCESAFSCFOKQOLKSANT 61

Db 30 QGQDRHMRQQLIDIVDQKNVNDLVPEFLPAPEDEVETNCWMSAFSCFOKAQLKSANT 89  
QY 62 GNNERIINVSIIKKLKRKPSTNAGRQKHRLTCDPSCDSEYKKPPKEFLERFKSLIQMIH 121  
Db 90 GNNERIINVSIIKKLKRKPSTNAGRQKHRLTCDPSCDSEYKKPPKEFLERFKSLIQMIH 149  
QY 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

RESULT 15  
US-11-174-398-2  
; Sequence 2, Application US/11174398  
; Publication No. US20050244930A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: West, James W.  
; APPLICANT: Novak, Julia E.  
; TITLE OF INVENTION: ZALPHAL1 LIGAND ANTAGONISTS  
; FILE REFERENCE: 01-37  
; CURRENT APPLICATION NUMBER: US/11/174,398  
; CURRENT FILING DATE: 2005-07-01  
; PRIOR APPLICATION NUMBER: US/10/282,622  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 60/337,586  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-174-398-2

Query Match 99.3%; Score 706; DB 6; Length 162;  
Best Local Similarity 100.0%; Pred. No. 4.7e-67;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QGQDRHMRQQLIDIVDQKNVNDLVPEFLPAPEDEVETNCWMSAFSCFOKAQLKSANT 61  
Db 30 QGQDRHMRQQLIDIVDQKNVNDLVPEFLPAPEDEVETNCWMSAFSCFOKAQLKSANT 89  
QY 62 GNNERIINVSIIKKLKRKPSTNAGRQKHRLTCDPSCDSEYKKPPKEFLERFKSLIQMIH 121  
Db 90 GNNERIINVSIIKKLKRKPSTNAGRQKHRLTCDPSCDSEYKKPPKEFLERFKSLIQMIH 149  
QY 122 QHLSRTHGSEDS 134  
Db 150 QHLSRTHGSEDS 162

Search completed: August 14, 2006, 21:56:26  
Job time : 180 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: August 14, 2006, 21:53:33 ; Search time 33 Seconds

(without alignment)  
273.328 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711

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Scoring table: BIOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: /EMC\_Celexra\_SIDS3/pcodara/1/pubppaa/US06\_NEW\_PUB pep.\*  
3: /EMC\_Celexra\_SIDS3/pcodara/1/pubppaa/US07\_NEW\_PUB pep.\*  
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8: /EMC\_Celexra\_SIDS3/pcodara/1/pubppaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	134	US-10-735-149-28	Sequence 28, Appl
2	706	99.3	162	US-10-511-937-2572	Sequence 2572, Ap
3	706	99.3	162	US-10-735-149-2	Sequence 2, Appl
4	706	99.3	162	US-10-806-611-10	Sequence 10, Appl
5	695	97.7	131	US-10-806-611-2	Sequence 2, Appl
6	524	73.7	122	US-10-806-611-12	Sequence 12, Appl
7	404	56.8	146	US-10-806-611-13	Sequence 13, Appl
8	394	55.4	122	US-10-806-611-4	Sequence 4, Appl
9	99.5	14.0	162	US-10-511-937-2499	Sequence 2499, Ap
10	74.5	10.5	431	US-11-056-355B-36356	Sequence 36356, A
11	74.5	10.5	431	US-11-056-355B-45283	Sequence 45283, A
12	74.5	10.5	441	US-11-056-355B-36355	Sequence 36355, A
13	74.5	10.5	441	US-11-056-355B-45282	Sequence 45282, A
14	74.5	10.5	463	US-11-056-355B-36354	Sequence 36354, A
15	74.5	10.5	463	US-11-056-355B-45281	Sequence 45281, A
16	71	10.0	555	US-11-056-355B-79971	Sequence 79971, A
17	71	10.0	631	US-11-056-355B-79970	Sequence 79970, A
18	70.5	9.9	864	US-11-056-355B-79969	Sequence 79969, A
19	70.5	9.9	352	US-11-056-355B-81843	Sequence 81843, A
20	70.5	9.9	565	US-10-471-571A-5038	Sequence 5038, Ap
21	70	9.8	861	US-10-520-470-73	Sequence 73, Appl
22	69.5	9.8	720	US-10-449-902-51542	Sequence 51542, A
23	69.5	9.8	864	US-11-251-208-77	Sequence 77, Appl
24	69	9.7	707	US-11-293-697-3241	Sequence 3241, Ap
25	68.5	9.6	212	US-11-056-355B-4865	Sequence 4865, Ap

26	68.5	9.6	247	US-11-056-355B-56995	Sequence 56995, A
27	68.5	9.6	335	US-11-056-355B-4864	Sequence 4864, Ap
28	68.5	9.6	417	US-11-056-355B-4863	Sequence 4863, Ap
29	68	9.6	320	US-11-056-355B-41014	Sequence 41014, A
30	68	9.6	328	US-11-056-355B-41013	Sequence 41013, A
31	68	9.6	1166	US-10-449-902-37528	Sequence 37528, A
32	67.5	9.5	378	US-11-053-349-32621	Sequence 32621, A
33	67.5	9.5	378	US-11-056-355B-64212	Sequence 64212, A
34	67.5	9.5	436	US-10-953-349-32620	Sequence 32620, A
35	67.5	9.5	436	US-11-056-355B-64211	Sequence 64211, A
36	67.5	9.5	461	US-10-953-349-32619	Sequence 32619, A
37	67.5	9.5	461	US-11-056-355B-64210	Sequence 64210, A
38	67.5	9.5	763	US-10-449-902-33868	Sequence 33868, A
39	67	9.4	179	US-10-449-902-49207	Sequence 49207, A
40	67	9.4	299	US-11-056-355B-20307	Sequence 20307, A
41	67	9.4	323	US-10-449-902-39494	Sequence 39494, A
42	67	9.4	617	US-11-056-355B-46959	Sequence 46959, A
43	67	9.4	619	US-11-056-355B-46958	Sequence 46958, A
44	66.5	9.4	171	US-10-953-349-16629	Sequence 16629, A
45	66	9.3	227	US-10-953-349-27717	Sequence 27717, A

## ALIGNMENTS

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RESULT 1
US-10-735-149-28
Sequence 28, Application US/10735149
Publication No. US20060134754A1
GENERAL INFORMATION:
APPLICANT: Chan, Chung
APPLICANT: Zamost, Bruce L.
APPLICANT: Covert, Douglas C.
APPLICANT: Liu, Hong Y.
APPLICANT: De Jongh, Karen S.
APPLICANT: Meyer, Jeffrey D.
APPLICANT: Holderman, Susan D.
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
TITLE OF INVENTION: IN A PROKARYOTIC HOST
FILE REFERENCE: 02-12
CURRENT APPLICATION NUMBER: US/10/735,149
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 134
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: optimized IL-21
US-10-735-149-28

Query Match      100.0%; Score 711; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 3e-62;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MCGQDRMIMRQLIDVDQKRYVNDLVPFLLPAPEDVETNCWMSFSCGQKQLKSAN 60
DB      1 MCGQDRMIMRQLIDVDQKRYVNDLVPFLLPAPEDVETNCWMSFSCGQKQLKSAN 60
QY      61 TGNNERIIVNSIKKLKKPKPSTNAGRQKRLTCCPSDSEYEKKPKPFLSRFKSLQKMI 120
DB      61 TGNNERIIVNSIKKLKKPKPSTNAGRQKRLTCCPSDSEYEKKPKPFLSRFKSLQKMI 120
QY      121 HOHLSRTHSEDS 134
DB      121 HOHLSRTHSEDS 134

RESULT 2
US-10-511-937-2572
Sequence 2572, Application US/10511937
Publication No. US2006008836A1

```

```

; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2572
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-511-937-2572

Query Match          99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,1e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||||
DB 30 QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 89
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QY 62 GNNERIINVSIKKLKRRPSTNAGRQKHRLTCPCSDSYEKKPPKEFLERFKSILQKMIH 121
    |||||||
DB 90 GNNERIINVSIKKLKRRPSTNAGRQKHRLTCPCSDSYEKKPPKEFLERFKSILQKMIH 149
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QY 122 QHLSRTHGSEDS 134
    |||||||
DB 150 QHLSRTHGSEDS 162
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RESULT 3
US-10-735-149-2
; Sequence 2, Application US/10735149
; Publication No. US20060134754A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Chung
; APPLICANT: Zamost, Bruce L.
; APPLICANT: Covert, Douglas C.
; APPLICANT: Liu, Hong Y.
; APPLICANT: De Jongh, Karen S.
; APPLICANT: Meyer, Jeffrey D.
; APPLICANT: Holderman, Susan D.
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21
; TITLE OF INVENTION: IN A PROKARYOTIC HOST
; FILE REFERENCE: 02-12
; CURRENT APPLICATION NUMBER: US/10/735,149
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-735-149-2

Query Match          99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,1e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 61
    |||||||
DB 30 QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 89
    |||||||
QY 62 GNNERIINVSIKKLKRRPSTNAGRQKHRLTCPCSDSYEKKPPKEFLERFKSILQKMIH 121
    |||||||
DB 90 GNNERIINVSIKKLKRRPSTNAGRQKHRLTCPCSDSYEKKPPKEFLERFKSILQKMIH 149
    |||||||
QY 122 QHLSRTHGSEDS 134
    |||||||
DB 150 QHLSRTHGSEDS 162
    |||||||

RESULT 4
US-10-806-611-10
; Sequence 10, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senices, Mayra
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806,611
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-806-611-10

Query Match          99.3%; Score 706; DB 6; Length 162;
Best Local Similarity 100.0%; Pred. No. 1,1e-61;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 61
    |||||||
DB 30 QGODRHMIIRNRQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKQKLSANT 89
    |||||||
QY 62 GNNERIINVSIKKLKRRPSTNAGRQKHRLTCPCSDSYEKKPPKEFLERFKSILQKMIH 121
    |||||||
DB 90 GNNERIINVSIKKLKRRPSTNAGRQKHRLTCPCSDSYEKKPPKEFLERFKSILQKMIH 149
    |||||||
QY 122 QHLSRTHGSEDS 134
    |||||||
DB 150 QHLSRTHGSEDS 162
    |||||||

RESULT 5
US-10-806-611-2
; Sequence 2, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Senices, Mayra
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806,611
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: US 60/456,920
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
```



SEQ ID NO 2  
LENGTH: 131  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-806-611-2

Query Match 97.7%; Score 695; DB 6; Length 131;  
Best Local Similarity 100.0%; Pred. No. 1e-60;  
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 63  
DB 1 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 60  
QY 64 NERIINVSIKKLKKRPSTNAGRQKHRLTQPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 123  
DB 61 NERIINVSIKKLKKRPSTNAGRQKHRLTQPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 120  
QY 124 LSSRTGSEDS 134  
DB 121 LSSRTGSEDS 131

RESULT 6  
US-10-806-611-12

Sequence 12, Application US/10806611  
Publication No. US20060159655A1

GENERAL INFORMATION:  
APPLICANT: Collins, Mary  
APPLICANT: Chin, Elaine Y.  
APPLICANT: Services, Mayra  
APPLICANT: Young, Deborah A.  
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF  
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR  
FILE REFERENCE: 16158-013001  
CURRENT APPLICATION NUMBER: US/10/806, 611  
CURRENT FILING DATE: 2004-03-22  
PRIOR APPLICATION NUMBER: US 60/456, 920  
PRIOR FILING DATE: 2003-03-21  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 12  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Bos taurus  
US-10-806-611-12

Query Match 73.7%; Score 524; DB 6; Length 122;  
Best Local Similarity 80.3%; Pred. No. 4.6e-44;  
Matches 98; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 4 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 63  
DB 1 QDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 60  
QY 64 NERIINVSIKKLKKRPSTNAGRQKHRLTQPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 123  
DB 61 NERIINVSIKKLKKRPSTNAGRQKHRLTQPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 120  
QY 124 LS 125  
DB 121 LS 122

RESULT 7

US-10-806-611-13  
Sequence 13, Application US/10806611  
Publication No. US20060159655A1

GENERAL INFORMATION:  
APPLICANT: Collins, Mary  
APPLICANT: Chin, Elaine Y.  
APPLICANT: Services, Mayra  
APPLICANT: Young, Deborah A.

TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF  
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR  
FILE REFERENCE: 16158-013001  
CURRENT APPLICATION NUMBER: US/10/806, 611  
CURRENT FILING DATE: 2004-03-22  
PRIOR APPLICATION NUMBER: US 60/456, 920  
PRIOR FILING DATE: 2003-03-21  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 13  
LENGTH: 146  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-806-611-13

Query Match 56.8%; Score 404; DB 6; Length 146;  
Best Local Similarity 62.1%; Pred. No. 2.9e-32;  
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 2 QGDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANT 61  
DB 23 QGDRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANT 82  
QY 62 GNERIINVSIKKLKKRPSTNAGRQKHRLTQPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 121  
DB 83 GNERIINVSIKKLKKRPSTNAGRQKHRLTQPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 142  
QY 122 QHLS 125  
DB 143 QHLS 146

RESULT 8

US-10-806-611-4  
Sequence 4, Application US/10806611  
Publication No. US20060159655A1

GENERAL INFORMATION:  
APPLICANT: Collins, Mary  
APPLICANT: Chin, Elaine Y.  
APPLICANT: Services, Mayra  
APPLICANT: Young, Deborah A.  
TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF  
TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR  
FILE REFERENCE: 16158-013001  
CURRENT APPLICATION NUMBER: US/10/806, 611  
CURRENT FILING DATE: 2004-03-22  
PRIOR APPLICATION NUMBER: US 60/456, 920  
PRIOR FILING DATE: 2003-03-21  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 4  
LENGTH: 122  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-806-611-4

Query Match 55.4%; Score 394; DB 6; Length 122;  
Best Local Similarity 62.0%; Pred. No. 2.2e-31;  
Matches 75; Conservative 19; Mismatches 27; Indels 0; Gaps 0;

QY 5 DRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 64  
DB 2 DRHMIRKQLIDIVDQKKNVNDLVPEFLPAPEDVETNCESAFSCFOKAOLKSANTGN 61  
QY 65 ERIINVSIKKLKKRPSTNAGRQKHRLTQPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 124  
DB 62 KTFIIVDVAQLRRRLPARBGKKQKHIAKPCSDSYEKKEPKFLEKFLERFKSLQKMIHQH 121  
QY 125 S 125  
DB 122 S 122

RESULT 9  
US-10-511-937-2499  
; Sequence 2499, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, Macdonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2499  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-511-937-2499

Query Match 14.0%; Score 99.5; DB 6; Length 162;  
Best Local Similarity 25.9%; Pred. No. 0.017;  
Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;

QY 15 IDIVDLKNTYNDLVPEF-----LPAPEDVETNCMSAFSCFQKQKSKANTGNNE 65  
Db 51 VNVISDJKK-IEDLIQSMHIDATLYTESDVHPSCVKYAMKCFLELQVISLESQDASIH 109  
QY 66 RIINVSIKKLKKRPSTNAGRRQKRLTSPSCDSYEKKRPKEFLERFKSLQKMIH 121  
Db 110 TWENLIT--LANNSSNGVNTS--GCKECELKEKNITEFLQSTVHIVOMFIN 160

RESULT 10  
US-11-056-355B-36356  
; Sequence 36356, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 36356  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(431)  
; OTHER INFORMATION: Ceres Seq. ID no. 13575998  
US-11-056-355B-36356

Query Match 10.5%; Score 74.5; DB 7; Length 431;  
Best Local Similarity 21.8%; Pred. No. 15;  
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY 6 RHMIRMQQLIDIVDLKNTYNDLVPEFLPAPEDVETNCMSAFSCFQKQKSKANTGNNE 65  
Db 220 KYKLARKKFLDVNPELQNSYNEVI-----APDIATYGGICALASFRRSLK-----Q 267  
QY 66 RIINVSIKKLKKRPSTNAGRRQKRLTSPSCDSYEKKRPKEFLERFKSLQKMIH 123  
Db 268 KVIDININFRNLELVPDRELINDFYSSRYASC-----LEYLASKSNLLDIDLHL 318

RESULT 11  
US-11-056-355B-45283  
; Sequence 45283, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 45283  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(431)  
; OTHER INFORMATION: Ceres Seq. ID no. 13575998  
US-11-056-355B-45283

Query Match 10.5%; Score 74.5; DB 7; Length 431;  
Best Local Similarity 21.8%; Pred. No. 15;  
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY 6 RHMIRMQQLIDIVDLKNTYNDLVPEFLPAPEDVETNCMSAFSCFQKQKSKANTGNNE 65  
Db 220 KYKLARKKFLDVNPELQNSYNEVI-----APDIATYGGICALASFRRSLK-----Q 267  
QY 66 RIINVSIKKLKKRPSTNAGRRQKRLTSPSCDSYEKKRPKEFLERFKSLQKMIH 123  
Db 268 KVIDININFRNLELVPDRELINDFYSSRYASC-----LEYLASKSNLLDIDLHL 318

RESULT 12  
US-11-056-355B-36355  
; Sequence 36355, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; TITLE OF INVENTION: Polypeptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 36355  
; LENGTH: 441  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(441)  
; OTHER INFORMATION: Ceres Seq. ID no. 13575997  
US-11-056-355B-36355

```

; OTHER INFORMATION: Ceres Seq. ID no. 13575996
US-11-056-355B-36354

Query Match      10.5%; Score 74.5; DB 7; Length 463;
Best Local Similarity 21.8%; Pred. No. 16;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY RHMI RMQLDIYDOLKNYVNDLVPEFLPAPDEVETNCESAFSCFOKAOLKSANTGNNE 65
Db KYTLAAKRPDLVPNELGNSYNEVI-----APDIAITGGICALASFPSRELK-----Q 299
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY RII-NVISIKTKKKRPPSTNAGRQKHRLTCPSCDSYEKKPKPFLEBFKSLIQMHIQH 123
Db KVIDINFRNFLVLVPVRELINDFYSSRYASC-----LBYIASLKSNLLLDIHILH 350
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 15
US-11-056-355B-45281
; Sequence 45281, Application US/11056355B
; Publication NO. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Alexander, Vyacheslav
TITLE OR INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1590P052
CURRENT APPLICATION NUMBER: US/11/056,355B
PRIOR FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ. ID NOS: 119966
SEQ ID NO 45281
LENGTH: 463
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: (1) .. (463)
OTHER INFORMATION: Ceres Seq. ID no. 13575996
US-11-056-355B-45281

Query Match      10.5%; Score 74.5; DB 7; Length 463;
Best Local Similarity 21.8%; Pred. No. 16;
Matches 26; Conservative 24; Mismatches 48; Indels 21; Gaps 4;

QY RHMI RMQLDIYDOLKNYVNDLVPEFLPAPDEVETNCESAFSCFOKAOLKSANTGNNE 65
Db KYTLAAKRPDLVPNELGNSYNEVI-----APDIAITGGICALASFPSRELK-----Q 299
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY RII-NVISIKTKKKRPPSTNAGRQKHRLTCPSCDSYEKKPKPFLEBFKSLIQMHIQH 123
Db KVIDINFRNFLVLVPVRELINDFYSSRYASC-----LBYIASLKSNLLLDIHILH 350
    :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Search completed: August 14, 2006, 21:57:05
Job time : 34 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2006, 21:42:58 ; Search time 195 Seconds

(without alignments)  
314.190 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711

Sequence: 1 MGGDRHMIRMQLIDIVDQ.....LLQKNHQLSSRTGSEDS 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	711	100.0	134	8	ADP70485
2	706	99.3	133	3	ADM43687
3	706	99.3	162	3	AAE18623
4	706	99.3	162	5	AAE13729
5	706	99.3	162	5	AAU11965
6	706	99.3	162	6	ABR61407
7	706	99.3	162	7	AAE14932
8	706	99.3	162	7	ABU62893
9	706	99.3	162	7	ADP17046
10	706	99.3	162	7	ADH44572
11	706	99.3	162	7	ADH44572
12	706	99.3	162	7	ADH44572
13	706	99.3	162	7	ADH44572
14	706	99.3	162	8	ADJ25621
15	706	99.3	162	8	ADM41017
16	706	99.3	162	8	ADP12563
17	706	99.3	162	8	ADP19731
18	706	99.3	162	8	ADP70459
19	706	99.3	162	8	ADP19031
20	706	99.3	162	8	ADP96355
21	706	99.3	162	9	ADY20419
22	706	99.3	162	9	ADY17792
23	706	99.3	162	9	ADZ20501

24	706	99.3	162	9	AEb26428	Human int
25	706	99.3	162	9	AEb68671	Human int
26	706	99.3	162	10	AEb19679	Human int
27	706	99.3	162	10	AEg05273	Human IL-
28	706	99.3	162	7	ADP17042	Human alb
29	696	97.9	160	9	AEa52828	Human int
30	695	97.7	131	8	ADs19023	Human int
31	695	97.7	131	8	ADw43684	Predicted
32	695	97.7	131	10	AEb19672	Human hu
33	695	97.7	519	3	AAE18627	Mature act
34	695	97.7	519	5	AAU11971	Amino aci
35	695	97.7	519	7	ADH44655	MBP-human
36	695	97.7	519	7	ADH44655	Human zal
37	695	97.7	519	8	ADP19814	MBP (malt
38	695	97.7	519	8	ADP19814	Human zal
39	694	97.6	162	7	AAE14934	Human int
40	694	97.6	162	8	ADY27249	Human int
41	661	93.0	133	9	ADw43680	Human int
42	656	92.3	133	9	ADw43682	Human int
43	650	91.4	131	9	ADw43678	Human int
44	645	90.7	131	9	ADw43674	Human int
45	645	90.7	131	9	ADw43672	Human int

## ALIGNMENTS

RESULT 1  
ADP70485  
ID ADP70485 standard; protein; 134 AA.  
XX  
AC ADP70485;  
DT 23-SEP-2004 (first entry)  
XX  
DE Codon optimised Interleukin 21 (IL-21) protein SEQ ID NO:28.  
XX  
KW Interleukin 21; IL-21; human; codon optimised.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS  
PN MO2004055168-A2.  
PD 01-JUL-2004.  
XX  
PF 12-DEC-2003; 2003WO-US039764.  
XX  
PR 13-DEC-2002; 2002US-0433448P.  
PR 13-DEC-2002; 2002US-0433452P.  
PA (ZYMO ) ZYMOGENETICS INC.  
PI Chang C, Zamost BL, Covert DC, Liu HY, De Jongh KS, Meyer JD;  
PI Holderman SD;  
PI  
PI WPI: 2004-500211/47.  
PI N-PSDB; ADP70484.  
XX  
XX New expression vectors for the large-scale production of IL-21 proteins  
XX comprises a prokaryotic origin of replication, a transcriptional  
XX initiation DNA element, a polynucleotide sequence and a transcriptional  
XX terminator.  
XX  
XX Claim 13; SEQ ID NO 28; 90pp; English.  
XX  
XX The present invention describes an expression vector for producing  
XX Interleukin 21 (IL-21) protein. The expression vector comprises the  
XX following operably linked elements: (a) a prokaryotic origin of  
XX replication; (b) a transcriptional initiation DNA element; (c) an IL-21  
XX polynucleotide sequence having the 405 base pair sequence given in SEQ ID  
XX NO:27 (ADP70484); and (d) a transcriptional terminator. Also described:  
XX (1) a prokaryotic host cell transformed with the expression vector

CC described above; (2) producing IL-21 proteins; (3) isolating insoluble IL-21 protein; and (4) a composition comprising an IL-21 protein comprising amino acids residues of the 134 amino acid sequence given in SEQ ID NO:28 (ADP70485) at a concentration of about 10 mg/ml IL-21 protein in 10 mM histidine, and 4.7 % mannitol at pH 5.3. The composition and methods are useful for the large-scale production of IL-21 in prokaryotic hosts. The CC present sequence represents a human IL-21 protein which has been codon optimized for prokaryotic expression, which is used in an example from the present invention.

XX  
CC  
XX  
SQ Sequence 134 AA;

Query Match 100.0%; Score 711; DB 8; Length 134;  
Best Local Similarity 100.0%; Pred. No. 1.le-73;  
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSAN 60  
DB 1 MOGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSAN 60  
QY 61 TGNERRIINVSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 120  
DB 61 TGNERRIINVSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 120  
QY 121 HQHLSRTHGSEDS 134  
DB 121 HQHLSRTHGSEDS 134

RESULT 2  
ADW43687 standard; protein; 133 AA.

XX  
AC ADW43687;

XX  
DT 24-MAR-2005 (first entry)

XX  
DE Mature human interleukin-21.

XX  
KW Interleukin-21; Antiallergic; Antiasthmatic; Antiparasitic;  
KW Antinflammatory; Neuroprotective; Cytostatic; Antimicrobial; allergy;  
KW Immune disorder; asthma; parasitic infection; inflammation;  
KW multiple sclerosis; cancer; neoplasm; infection.

XX  
OS Homo sapiens.

XX  
PN WO2004112703-A2.

XX  
PD 29-DEC-2004.

XX  
PF 15-JUN-2004; 2004WO-US018903.

XX  
PR 19-JUN-2003; 2003US-0479772P.

XX  
PA (CENZ ) CENTOCOR INC.

XX  
PI Cunningham MR, Heaven GA, Luo J, Song XR;

XX  
DR WPI; 2005-048751/05.

XX  
DR N-PSDB; ADW43686.

XX  
PT New polynucleotides encoding interleukin-21 analogs, useful for treating  
PT allergic diseases as well as asthma, parasitic diseases, inflammatory  
PT diseases (e.g. multiple sclerosis), cancer, or infectious diseases.

XX  
PS Claim 4; SEQ ID NO 19; 28pp; English.

XX  
CC The invention relates to an isolated polynucleotides encoding interleukin-21 analogs. Also included are the interleukin-21 analog proteins, a vector comprising the polynucleotide, an isolated host cell comprising the vector and a process for producing a polypeptide comprising culturing the host cell under conditions for production of the polypeptide. The CC polynucleotides and polypeptides, composition and method are useful for

CC treating allergic diseases as well as asthma, parasitic diseases,  
CC inflammatory diseases such as multiple sclerosis, cancer, or infectious  
CC diseases. The present sequence represents the wild-type mature human IL-21.

XX  
SQ Sequence 133 AA;

Query Match 99.3%; Score 706; DB 9; Length 133;  
Best Local Similarity 100.0%; Pred. No. 4e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 OGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSANT 61  
DB 1 OGDRHMRKQLIDVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKQLKSANT 60  
QY 62 GNNERRIINVSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 121  
DB 61 GNNERRIINVSIKKLKKRPSTNAGRRQKRLTSPSCDSYKKPKPEFLERFKSLQKMI 120  
QY 122 QHLSRTHGSEDS 134  
DB 121 QHLSRTHGSEDS 133

RESULT 3  
AAB18623 standard; protein; 162 AA.

XX  
AC AAB18623;

XX  
DT 22-JAN-2001 (first entry)

XX  
DE A human zalphal1 ligand polypeptide.

XX  
KW zalphal1 ligand; cytokine; haematopoietic cell proliferation; lymphoma;  
KW tumorigenesis; leukaemia; hematopoiesis; B cell tumour.

XX  
OS Homo sapiens.

XX  
PN WO200053761-A2.

XX  
PD 14-SEP-2000.

XX  
PF 09-MAR-2000; 2000WO-US006067.

XX  
PR 09-MAR-1999; 99US-00264908.

XX  
PR 11-MAR-1999; 99US-00265992.

XX  
PR 01-JUL-1999; 99US-0142013P.

XX  
PA (ZYMO ) ZYMOGENETICS INC.

XX  
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

XX  
DR Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX  
DR WPI; 2000-565600/52.

XX  
DR N-PSDB; AAA75552.

XX  
PT New human cytokine, designated zalphal1 ligand, useful for stimulating  
PT the proliferation and/or development of hematopoietic cells in vitro and  
PT in vivo, and for treating tumorigenesis.

XX  
PS Disclosure; Page 205-206; 256pp; English.

XX  
CC The present sequence represents a human zalphal1 ligand polypeptide,  
CC which is a cytokine. The zalphal1 ligand is useful for stimulating the  
CC proliferation and development of haematopoietic cells in vitro and in  
CC vivo. Zalphal1 ligand polynucleotides can be used as primers or probes  
CC for cloning the zalphal1 gene. The zalphal1 ligand is useful for treating  
CC tumorigenesis. A zalphal1 ligand-saporin fusion toxin may be used for  
CC treating leukaemias and lymphomas. Antagonists against zalphal1 ligand  
CC are useful as research reagents for characterizing ligand-receptor  
CC interaction. Antagonists are also useful for inhibiting expansion,  
CC proliferation, activation and differentiation of cells involved in

CC regulating hematopoiesis. The zalphall ligand may also be used to  
 CC stimulate an immune response against B cell tumour, a virus, a parasite  
 CC or a bacterium. The zalphall polypeptides, polynucleotides, antagonists,  
 CC agonists and antibodies are also useful for the detection, diagnosis,  
 CC prevention, and treatment of diseases associated with a zalphall ligand  
 CC genetic defect

XX Sequence 162 AA;

Query Match 99.3%; Score 706; DB 3; Length 162;

Best Local Similarity 100.0%; Pred. No. 5.2e-73; Indels 0; Gaps 0;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMRMQLIDIVQLKNVNDLVEFLPADEVETNCMSAFSCFOKAQKSNANT 61  
 DB 30 QGDRHMRMQLIDIVQLKNVNDLVEFLPADEVETNCMSAFSCFOKAQKSNANT 89  
 QY 62 GNNERIIVSIKIKLRKPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121  
 DB 90 GNNERIIVSIKIKLRKPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149  
 QY 122 QHLSRRTGSEDS 134  
 DB 150 QHLSRRTGSEDS 162

RESULT 4

AAE13729

ID AAE13729 standard; protein; 162 AA.

AC AAE13729;

DT 26-FEB-2002 (first entry)

DE Human soluble Zalphall cytokine receptor ligand protein.

XX Human; Zalphall; cytokine receptor; immunosuppressive; cytostatic;  
 KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
 KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;  
 KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;  
 KW viral infection.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..31 /label= Signal\_peptide

FT Protein 32..162 /label= Mature\_zalphall\_ligand

FT Region 41..56 /label= Helix\_A

FT Region 69..84 /label= Helix\_B

FT Region 92..105 /label= Helix\_C

FT Region 135..148 /label= Helix\_D

FT Region 136..138 /note= "Conserved region"

XX MO200177171-A2.

XX 18-OCT-2001.

XX 03-APR-2001; 2001WO-US010872.

XX 05-APR-2000; 2000US-0194731P.

XX 28-JUL-2000; 2000US-0222121P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;

XX WPI; 2002-025898/03.  
 DR N-PSDB; AAD22923.

PT Novel soluble receptor polypeptides and polynucleotides used as cytokine  
 PT antagonist for stimulating ligand activity-induced proliferation of  
 PT hematopoietic cells and for suppressing immune response in a mammal.

XX Claim 1; Page 181; 243pp; English.

CC The invention relates to an isolated soluble zalphall cytokine receptor  
 CC polypeptide and their cDNA molecules. Zalphall proteins are useful for  
 CC inhibiting or antagonizing the ligand activity-induced proliferation of  
 CC haematopoietic cells and haematopoietic cell progenitors preferably  
 CC lymphoid cells which are natural killer cells or cytotoxic T cells.  
 CC Zalphall is useful for treating immune and inflammatory disorders, for  
 CC reducing proliferation of neoplastic B or T cells, for suppressing an  
 CC immune response in a mammal exposed to an antigen or pathogen. Zalphall is  
 CC useful for treating diseases that require immune regulation including  
 CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,  
 CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;  
 CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,  
 CC sepsis, viral infection (dengue virus infection) and cancer. The present  
 CC sequence is human soluble zalphall cytokine receptor ligand

SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 5; Length 162;

Best Local Similarity 100.0%; Pred. No. 5.2e-73; Indels 0; Gaps 0;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMRMQLIDIVQLKNVNDLVEFLPADEVETNCMSAFSCFOKAQKSNANT 61  
 DB 30 QGDRHMRMQLIDIVQLKNVNDLVEFLPADEVETNCMSAFSCFOKAQKSNANT 89  
 QY 62 GNNERIIVSIKIKLRKPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121  
 DB 90 GNNERIIVSIKIKLRKPSTNAGRQKRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149  
 QY 122 QHLSRRTGSEDS 134  
 DB 150 QHLSRRTGSEDS 162

RESULT 5

AAU1965

ID AAU1965 standard; protein; 162 AA.

AC AAU1965;

DT 09-APR-2002 (first entry)

DE Human zalphall ligand polypeptide.

XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;  
 KW natural killer cell proliferation; T-cell proliferation;  
 KW B-cell proliferation; anti-tumour response; immune system;  
 KW immunostimulant; cytostatic; human; hPBCS;  
 KW activated human peripheral blood cell.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..31 /label= Signal\_peptide

FT Protein 32..162 /label= Mature\_zalphall\_ligand

XX US6307024-B1.

XX 23-OCT-2001.

XX 09-MAR-2000; 2000US-00522217.

XX 09-MAR-1999; 99US-0123547P.  
PR 11-MAR-1999; 99US-0123904P.  
PR 01-JUL-1999; 99US-0142013P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;  
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
XX  
DR WPI: 2002-0040208/05.  
DR N-PSDB; AAS20637.  
XX  
PT New zalphall ligand polypeptides and polynucleotides, useful for  
PT stimulating proliferation, activation, differentiation and/or induction  
PT of inhibition of specialized cell function, or for stimulating an  
PT antigenic response.  
XX  
PS Claim 7, Col 125-126; 105pp; English.  
XX  
CC The present invention relates to the isolation of a novel cytokine,  
CC zalphall ligand and the polynucleotide encoding it. The invention also  
CC gives the sequence for the zalphall receptor and the polynucleotide  
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of  
CC natural killer (NK) cells or NK cell progenitors, the activation of NK  
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with  
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and  
CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The  
CC zalphall ligand polypeptide is also useful in preparing antibodies that  
CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can  
CC be used as probes or primers to clone regions of a zalphall ligand gene,  
CC and in gene therapy. Zalphall ligand may also be used to identify  
CC inhibitors of its activity, to enhance the generation of anti-tumour  
CC responses with or without the infusion of donor lymphocytes, and to  
CC activate or stimulate the immune system. The present sequence represents  
CC human zalphall ligand polypeptide. The cDNA encoding this is isolated  
CC from a cDNA library from activated human peripheral blood cells (hPBcs)  
XX  
SQ Sequence 162 AA;  
XX  
Query Match 99.3%; Score 706; DB 5; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QGODRHIMRQRLDIYDQKKNVNDLVPEFLPAPEDEVETNCESASFCQKQKLSANT 61  
DB 30 QGODRHIMRQRLDIYDQKKNVNDLVPEFLPAPEDEVETNCESASFCQKQKLSANT 89  
QY 62 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121  
DB 90 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149  
QY 122 QHLSRTHGSEDS 134  
DB 150 QHLSRTHGSEDS 162  
XX  
RESULT 6  
ABR61407  
ID ABR61407 standard; protein: 162 AA.  
XX  
AC ABR61407;  
XX  
DT 12-AUG-2003 (first entry)  
XX  
DE Human IL-21 SEQ ID NO:19.  
XX  
KW arthritic disorder; interleukin-21; IL-21; IL-21 receptor; IL-21R;  
KW immune cell activity; cancer; infectious disorder; antineoplastic;  
KW antineoplastic; osteoporosis; antiparasitic; cytosolic; antibacterial;  
KW virucide; antiparasitic; immunosuppressive; antidiabetic; dermatological;  
KW neuroprotective; antitumor; antiallergic; antineoplastic; hepatotropic;  
KW antithyroid; antiinflammatory; immune response; immune disorder;

KW autoimmune disease; human.  
XX  
XX Homo sapiens.  
OS  
XX WO2003028630-A2.  
PN  
XX  
PD 10-APR-2003.  
XX  
PF 04-OCT-2002; 2002WO-US029839.  
XX  
PR 04-OCT-2001; 2001US-00972218.  
PR 17-APR-2002; 2002US-0373746P.  
XX  
XX (AMHP ) WYETH.  
PA  
PI Carter L, Whitters MJ, Collins M, Young DA, Larsen G;  
PI Donaldson DD, Lowe JD, Dunne K, Ma M, Witke JS, Kasalan MT;  
PI Ungar M;  
XX  
XX WPI: 2003-430146/40.  
XX  
DR N-PSDB; ACC80873.  
XX  
PT Treating or preventing arthritic disorder, cancer or infectious disorders  
PT in a subject, involves administering a modulator of interleukin-21 or its  
PT receptor which modulate immune cell activity.  
XX  
PS Disclosure; Page 37; 176pp; English.  
XX  
CC The invention relates to a novel method for treating or preventing an  
CC arthritic disorder in a subject. The method involves administering to the  
CC subject an interleukin-21 (IL-21)/IL-21 receptor (IL-21R) antagonist  
CC optionally in combination with another therapeutic agent, to inhibit or  
CC reduce immune cell activity in the subject. The method is also useful for  
CC treating or preventing cancer or an infectious disorder, in a subject, by  
CC administering IL-21/IL-21R agonist, to increase immune cell activity. The  
CC method of the invention has antirheumatic, antiarthritic, osteopathic,  
CC antiparasitic, cytostatic, antibacterial, virucide, antiparasitic,  
CC immunosuppressive, antidiabetic, neuroprotective, dermatological,  
CC antitumor, antineoplastic, antiallergic, antineoplastic, hepatotropic,  
CC antithyroid, and antiinflammatory activity. The method is useful for  
CC treating or preventing an arthritic disorder such as rheumatoid  
CC arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic  
CC arthritis or ankylosing spondylitis, and also cancer such as solid  
CC tumour, soft tissue tumour or metastatic lesion, or an infectious  
CC disorder such as a bacterial, viral or parasitic infection in a mammal,  
CC preferably human. A method of the invention is also useful for  
CC increasing the ability of a vaccine composition containing an antigen to  
CC elicit a protective immune response in a subject against the antigens.  
CC The antigen is from a pathogen such as virus, bacterium or protozoan, or  
CC from cancer or tumour cell antigen, or expressed on the surface of cancer  
CC cell. An alternative method of the invention is useful for modulating the  
CC activity of immune or haematopoietic cells and thus to treat or prevent a  
CC variety of immune disorders, such as autoimmune diseases, for example  
CC diabetes mellitus, multiple sclerosis, myasthenia gravis, systemic lupus  
CC erythematosus, dermatitis, ulcer, asthma, allergic asthma, anaemia,  
CC hepatitis, Graves's disease, graft versus host disease, and scleroderma.  
CC The present sequence is used in an exemplification of the invention  
XX  
SQ Sequence 162 AA;  
XX  
Query Match 99.3%; Score 706; DB 6; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QGODRHIMRQRLDIYDQKKNVNDLVPEFLPAPEDEVETNCESASFCQKQKLSANT 61  
DB 30 QGODRHIMRQRLDIYDQKKNVNDLVPEFLPAPEDEVETNCESASFCQKQKLSANT 89  
QY 62 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 121  
DB 90 GNNERIINVSIIKKLKRKPPSTNAGRQKHRLTSPSCDSYEKKPKPEFLERFKSLIQKMIH 149  
QY 122 QHLSRTHGSEDS 134



Db 150 QHLSRTHGSEDS 162

|||||

RESULT 7

AAE14932

ID AAE14932 standard; protein; 162 AA.

XX AAE14932;

XX 27-AUG-2003 (first entry)

XX Human interleukin-21 (IL-21).

DE Interleukin-21; IL-21; antagonist; cancer; inflammatory;

XX autoimmune disorder; rheumatoid arthritis; multiple sclerosis;

KM systemic lupus erythematosus; myasthenia gravis; diabetes; human;

XX zaiaphall ligand.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 41..56

FT Binding-site /label= Helix\_A

FT Binding-site 44

FT /note= "Important for IL-21 binding to its receptor"

FT Region 57..68

FT /label= A/B\_loop

FT Region 69..84

FT /label= Helix\_B

FT Region 85..91

FT /label= B/C\_loop

FT Region 92..105

FT /label= Helix\_C

FT Region 106..134

FT /label= C/D\_loop

FT Region 135..148

FT /label= Helix\_D

FT Binding-site 135

FT /note= "Important for IL-21 binding to its receptor"

PN WO2003040313-A2.

XX 15-MAY-2003.

XX 28-OCT-2002; 2002WO-US034502.

XX 05-NOV-2001; 2001US-0337586P.

XX (ZIMO ) ZYMOGENETICS INC.

XX Presnell SR, West JW, Novak JE;

XX WPI: 2003-441547/41.

XX N-PSDB; AAD47852.

XX New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing

PT and treating disorders with aberrant expression or activity of the IL-21

PT polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and

PT diabetes.

PS Disclosure; Page 53-54; 71pp; English.

XX The invention relates to polynucleotides and polypeptides of interleukin-

CC 21 (IL-21) antagonists, that bind with specificity and exhibit an EC50

CC that is not detectable in receptor binding studies. The antagonists of

CC the invention have mutations in the D helix of the IL-21 molecule, and

CC can be used to inhibit the activity of IL-21 with its cognate receptor.

CC The IL-21 antagonists are useful for diagnosing and treating disorders

CC involving the aberrant expression or activity of the IL-21 polypeptide,

CC such as cancer, inflammatory and autoimmune disorders, including

CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,

CC myasthenia gravis and diabetes. The polypeptides can also be used to

CC prepare antibodies that bind IL-21 epitopes, peptides or polypeptides,

CC and for enhancing in vivo killing of target tissues. The present sequence

CC is human IL-21 (originally designated zaiaphall ligand)

XX

SQ Sequence 162 AA;

Query Match 99.3%; Score 706; DB 7; Length 162;

Best Local Similarity 100.0%; Pred. No. 5,2e-73;

Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGDRHMIKRMQLIDIVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKAQLKSANT 61

Db 30 QGDRHMIKRMQLIDIVDLKNVNDLVPEFLPAPEDEVETNCWSAFSCFOKAQLKSANT 89

QY 62 GNNERIINVSIKKIKRRPPTNAGRQKRLTCSGDSYEKKPPEPLERKSLIQKMIH 121

Db 90 GNNERIINVSIKKIKRRPPTNAGRQKRLTCSGDSYEKKPPEPLERKSLIQKMIH 149

QY 122 QHLSRTHGSEDS 134

Db 150 QHLSRTHGSEDS 162

RESULT 8

ABU62893

ID ABU62893 standard; protein; 162 AA.

XX ABU62893;

XX 15-SEP-2003 (first entry)

XX Human interleukin 21 (IL-21).

DE Human; MU-1; haematopoietin receptor superfamily chain; immunomodulator;

XX cytosolic; antibacterial; virucide; antianaemic; gene therapy;

KM haematopoiesis; anaemias; immune response; cancer; infection;

XX transplanted organ; cytokine; receptor; interleukin 21; IL21.

OS Homo sapiens.

XX US2003049798-A1.

XX 13-MAR-2003.

XX 04-OCT-2001; 2001US-00972218.

XX 17-MAR-1998; 98US-00040005.

XX 28-APR-2000; 2000US-00560766.

XX 11-MAY-2000; 2000US-00569384.

XX (CART/) CARTER L.

XX (WHIT/) WHITTERS M J.

XX (COLL/) COLLINS M.

XX (YOUNG/) YOUNG D A.

XX (DONA/) DONALDSON D D.

XX (LOWE/) LOWE L D.

XX (UNGE/) UNGER M.

XX Carter L, Whitters MJ, Collins M, Young DA, Donaldson DD;

XX Lowe LD, Unger M;

XX WPI: 2003-513354/48.

XX N-PSDB; ACD26729.

XX New fusion polypeptide for regulating hematopoiesis and immune responses,

PT comprises a fragment of a MU-1 polypeptide and a non-MU-1 fusion

PT polypeptide.

PS Disclosure; Page 10; 26pp; English.

XX The invention describes a fusion polypeptide comprising at least a

CC fragment of a WT-1 polypeptide and a non-WT-1 fusion polypeptide. The  
CC polypeptide is useful in regulating haematopoiesis (e.g. in cases of  
CC anaemias) and/or immune responses (e.g. immune response to cancer,  
CC infections or to a transplanted organ) and in identifying other members  
CC of the haematopoietin superfamily, including cytokines and receptors. The  
CC polynucleotide may be used to express recombinant protein for analysis,  
CC characterisation or therapeutic use; and as markers for tissues or  
CC chromosomes. The polypeptide and polynucleotide may also be used as  
CC nutritional sources or supplements. This is the amino acid sequence of  
CC human interleukin 21 (IL21), a cytokine receptor that can be used to  
CC characterise the novel haematopoietin receptor of the invention  
SQ Sequence 162 AA;  
QY Query Match 99.3%; Score 706; DB 7; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 2 QGODRHMIRMROLIDIVDQKNYNDLVPEFLPAPEDEVETNCMSAFSCFOKAOLKSANT 61  
30 QGODRHMIRMROLIDIVDQKNYNDLVPEFLPAPEDEVETNCMSAFSCFOKAOLKSANT 89  
QY 62 GNNERRIINVSIKKLRKRPSTNAGRQKRLTSPSCSYEKPKPEFLERFKSILQRMH 121  
90 GNNERRIINVSIKKLRKRPSTNAGRQKRLTSPSCSYEKPKPEFLERFKSILQRMH 149  
QY 122 QHLSRTHGSEDS 134  
150 QHLSRTHGSEDS 162  
DB ADEB85808 standard; protein; 162 AA.  
RESULT 9  
ADEB85808  
ID ADEB85808 standard; protein; 162 AA.  
XX ADEB85808;  
DT 29-JAN-2004 (first entry)  
XX Human interleukin-21.  
DE Human interleukin-21;  
XX Human; interleukin-21; immunosuppressive; antirheumatic; antiarthritic;  
KW antiinflammatory; dermatological; ophthalmological; uropathic;  
KW muscular-gen.; vasotrophic; antidiabetic; anticholesteric; thyromimetic;  
KW neuroprotective; gastrointestinal-gen.; antiporiatic; gene therapy.  
XX Homo sapiens.  
OS  
XX WO2003087320-A2.  
PN  
XX 23-OCT-2003.  
PD  
XX 08-APR-2003; 2003WO-US010736.  
PF  
XX 09-APR-2002; 2002US-0371038P.  
PR  
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA  
XX Moll T, Strom TB, Zheng XX;  
XX Moll T, Strom TB, Zheng XX;  
XX WPI; 2003-845317/78.  
DR  
XX New substantially pure interleukin-21 polypeptide, useful for diagnosing,  
PT treating and prognosticating autoimmune disorders, e.g. rheumatic  
PT disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis  
PT and myasthenia gravis.  
PS  
XX Disclosure; SEQ ID NO 1; 65pp; English.  
XX The present sequence is the protein sequence of human interleukin-21 (IL-  
CC 21). The invention provides antagonists of the IL-21 receptor. These  
CC include mutants of murine IL-21 in which the Gln residue at position 119  
CC of the mature polypeptide is substituted by Asp or in which the Gln  
CQ

CC residues at positions 114 and 119 of the mature polypeptide are both  
CC replaced by Asp. The mutant IL-21 polypeptides inhibit or suppress T-cell  
CC activation. They preferably comprise a sequence that increases  
CC circulating half-life, such as the FC region of an IgG molecule and may  
CC further comprise an antigenic tag. Such antagonists inhibit cellular  
CC proliferation in response to either anti-CD3 monoclonal antibodies or  
CC anti-CD3 antibodies applied together with IL-2 and/or IL-15 together with  
CC IL-21. A claimed method of suppressing the immune response in a patient  
CC comprises administering the IL-21 antagonist or a nucleic acid encoding  
CC it. The method is used to treat an autoimmune disease such as rheumatic  
CC disease, including systemic lupus erythematosus, Sjogren's syndrome,  
CC scleroderma, mixed connective tissue disease, dermatomyositis,  
CC polymyositis, Reiter's syndrome, or Bence's disease, or rheumatoid  
CC arthritis, type I diabetes, autoimmune disease of the thyroid such as  
CC Hashimoto's thyroiditis or Graves' disease, an autoimmune disease of the  
CC central nervous system such as multiple sclerosis, myasthenia gravis, or  
CC encephalomyelitis, or an autoimmune disease selected from pemphigus  
CC vulgaris, pemphigus vegetans, pemphigus foliaceus, Senear-Usher syndrome,  
CC Brazilian pemphigus, psoriasis or inflammatory bowel disease (all  
CC claimed).  
SQ Sequence 162 AA;  
QY Query Match 99.3%; Score 706; DB 7; Length 162;  
Best Local Similarity 100.0%; Pred. No. 5.2e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 2 QGODRHMIRMROLIDIVDQKNYNDLVPEFLPAPEDEVETNCMSAFSCFOKAOLKSANT 61  
30 QGODRHMIRMROLIDIVDQKNYNDLVPEFLPAPEDEVETNCMSAFSCFOKAOLKSANT 89  
QY 62 GNNERRIINVSIKKLRKRPSTNAGRQKRLTSPSCSYEKPKPEFLERFKSILQRMH 121  
90 GNNERRIINVSIKKLRKRPSTNAGRQKRLTSPSCSYEKPKPEFLERFKSILQRMH 149  
QY 122 QHLSRTHGSEDS 134  
150 QHLSRTHGSEDS 162  
DB ADEB85808 standard; protein; 162 AA.  
RESULT 10  
ADEB85808  
ID ADEB85808 standard; protein; 162 AA.  
XX ADEB85808;  
DT 12-FEB-2004 (first entry)  
XX Human albumin fusion protein-related protein SeqID2177.  
DE Human albumin fusion protein-related protein SeqID2177.  
XX albumin fusion protein; albumin activity; human serum albumin;  
KW serum osmotic pressure; shelf-life; stability; antidiabetic;  
KW gene therapy; diabetes mellitus; human; gene; de.  
XX Homo sapiens.  
OS  
XX WO2003060071-A2.  
PN  
XX 24-JUL-2003.  
PD  
XX 23-DEC-2002; 2002WO-US040891.  
PF  
XX 21-DEC-2001; 2001US-0341811P.  
PR 26-JAN-2002; 2002US-0350358P.  
PR 26-JAN-2002; 2002US-0351360P.  
PR 26-FEB-2002; 2002US-0359370P.  
PR 28-FEB-2002; 2002US-0360000P.  
PR 27-MAR-2002; 2002US-0367500P.  
PR 08-APR-2002; 2002US-0370227P.  
PR 10-MAY-2002; 2002US-0378950P.  
PR 24-MAY-2002; 2002US-0382617P.  
PR 28-MAY-2002; 2002US-0383123P.  
PR 05-JUN-2002; 2002US-0385708P.  
CQ

PR 10-JUL-2002; 2002US-0394625P.  
 PR 24-JUL-2002; 2002US-0398008P.  
 PR 09-AUG-2002; 2002US-0402131P.  
 PR 13-AUG-2002; 2002US-0402708P.  
 PR 18-SEP-2002; 2002US-0411355P.  
 PR 18-SEP-2002; 2002US-0411426P.  
 PR 02-OCT-2002; 2002US-0414984P.  
 PR 11-OCT-2002; 2002US-0417611P.  
 PR 23-OCT-2002; 2002US-0420246P.  
 PR 05-NOV-2002; 2002US-0423623P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (DELZ) DELTA BIOTECHNOLOGY LTD.  
 PA (PRIN-) PRINCIPAL PHARM CORP.  
 XX  
 PI Balance DJ, Turner AJ, Rosen CA, Haseltine WA;  
 XX  
 DR WPI; 2003-598517/56.  
 DR N-PSDB; ADF17040.  
 XX  
 PT New albumin fusion protein, useful for preparing a composition for  
 treating diabetes mellitus.  
 XX  
 PS Example 4; SEQ ID NO 2177; 24pp; English.  
 XX  
 CC This invention relates to a novel albumin fusion protein having albumin  
 or biological activity. Human serum albumin is responsible for a  
 significant proportion of the osmotic pressure of serum and also  
 functions as a carrier of endogenous and exogenous ligands. The fusion of  
 albumin to a therapeutic protein may increase shelf-life and stability of  
 the therapeutic protein. The albumin fusion protein of the invention may  
 allow production of compositions with antidiabetic activity whilst the  
 nucleotide sequence which encodes it may be useful for gene therapy. The  
 albumin fusion protein is useful for preparing a composition for treating  
 diabetes mellitus. The present sequence is that of a therapeutic protein  
 which was fused with human albumin to create a novel albumin fusion  
 protein of the invention. Note: The sequence data for this patent did not  
 form part of the printed specification, but was obtained in electronic  
 format directly from WIPO at ftp.wipo.int/pub/publishedpat\_sequences  
 XX  
 SQ Sequence 162 AA;  
 Query Match 99.3%; Score 706; DB 7; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5,2e-73;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QGQDRHMRKQRLIDIVQLKNNYNDLVPEFLPAPDEVETNCESAFSCFQKQKLSANT 61  
 DB 30 QGQDRHMRKQRLIDIVQLKNNYNDLVPEFLPAPDEVETNCESAFSCFQKQKLSANT 89  
 QY 62 GNNRRIINVSIKKIKRKPSTNAGRQKRLTCPSCDSEYKKPKPEPLERKSLQKKI 121  
 DB 90 GNNRRIINVSJKKIKRKPSTNAGRQKRLTCPSCDSEYKKPKPEPLERKSLQKKI 149  
 QY 122 QHLSRTGSEDS 134  
 DB 150 QHLSRTGSEDS 162  
 RESULT 11  
 ADH44572  
 ID ADH44572 standard; protein, 162 AA.  
 AC ADH44572;  
 XX  
 DT 25-MAR-2004 (first entry)  
 XX  
 DE Human zalphall ligand protein.  
 XX  
 KW Human; Zalphall ligand; Zalphall receptor; immune response;  
 tumour progression; metastasis; tumour stasis; haematopoietic tumour;  
 lymphoma; B cell tumour; systemic lupus erythematosus;  
 rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease;

KW Immunocompromised patient; HIV infection; vaccine; chromosome 4q27.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..31  
 FT /note= "Signal peptide"  
 FT Protein 32..162  
 FT /note= "Mature Zalphall, claimed in claim 1"  
 XX  
 FN US6605272-B2.  
 XX  
 PD 12-AUG-2003.  
 XX  
 PF 03-AUG-2001; 2001US-00923246.  
 XX  
 PR 09-MAR-1999; 99US-0123547P.  
 PR 11-MAR-1999; 99US-0123904P.  
 PR 01-JUL-1999; 99US-0142013P.  
 PR 09-MAR-2000; 2000US-00522217.  
 XX  
 PA (ZYMO) ZYMOGENETICS INC.  
 XX  
 PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;  
 PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
 DR WPI; 2003-895283/82.  
 XX  
 PT Stimulating an immune response in a mammal exposed to an antigen or  
 pathogen, useful for enhancing anti-tumor activity resulting in reduced  
 tumor progression or metastasis, comprises administering zalphall ligand  
 polypeptide.  
 PT  
 PS Claim 1; SEQ ID NO 2; 103pp; English.  
 XX  
 CC The invention relates to stimulating an immune response in a mammal  
 exposed to an antigen or pathogen comprising administering a composition  
 comprising mature zalphall ligand polypeptide comprising residues 32-162  
 of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an  
 immune response in a mammal exposed to an antigen or pathogen  
 (comprising: (a) determining (indirectly the level of antigen or  
 pathogen present in the mammal; (b) administering a composition  
 comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c)  
 determining (indirectly the level of antigen or pathogen in the mammal;  
 and (d) comparing the antigen or pathogen level in (a) with (b), where a  
 change in the level indicates stimulation of immune response), and  
 stimulating an immune response in a mammal exposed to an antigen or  
 pathogen (comprising: (a) determining a level of antigen- or pathogen-  
 specific antibody; (b) administering a composition comprising zalphall  
 ligand polypeptide in a pharmaceutical vehicle; (c) determining a post  
 administration level of the antigen- or pathogen-specific antibody; and  
 (d) comparing the level of the antibody in (a) with (b), where an  
 increase in the antibody level indicates stimulation of immune response).  
 CC The method is useful for stimulating an immune response in a mammal  
 exposed to an antigen or pathogen, and for enhancing anti-tumour activity  
 resulting in a reduction in tumour progression, decrease in metastasis,  
 or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma  
 or a B cell tumour. The zalphall ligand is useful for treating a wide  
 range of diseases arising from defects in the immune system, e.g.  
 systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or  
 diabetes, for boosting immunity to infectious diseases, treating  
 immunocompromised patients, such as HIV+ patients and in improving  
 vaccines. The present sequence is a human zalphall ligand protein.  
 XX  
 SQ Sequence 162 AA;  
 Query Match 99.3%; Score 706; DB 7; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 5,2e-73;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QGQDRHMRKQRLIDIVQLKNNYNDLVPEFLPAPDEVETNCESAFSCFQKQKLSANT 61  
 DB 30 QGQDRHMRKQRLIDIVQLKNNYNDLVPEFLPAPDEVETNCESAFSCFQKQKLSANT 89

```
QY 62 GNNERIINVSISKLLKRRKPSTNAGRQKHRLTCPSCSYKKPKPEFLERFKSLLOQMIIH 121
DB 90 GNNERIINVSISKLLKRRKPSTNAGRQKHRLTCPSCSYKKPKPEFLERFKSLLOQMIIH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162

RESULT 12
AD100908
ID AD100908 standard; protein; 162 AA.
XX
XX AD100908;
XX
XX 22-APR-2004 (first entry)
XX
DE Immunity-related human zai1phal1 ligand protein.
XX
KM zai1phal1 ligand; immunity; infectious disease; immunocompromised patient;
XX HIV; vaccine; human.
XX
OS Homo sapiens.
XX
XX US2003125524-A1.
XX
XX 03-JUL-2003.
XX
XX 15-NOV-2002; 2002US-00295723.
XX
XX 09-MAR-2000; 2000US-00522217.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD,
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
XX WPI; 2003-811003/76.
XX
XX N-PSDB; AD100907.
XX
XX
XX New zai1phal1 ligand polypeptides, useful for boosting immunity to
XX infectious diseases, and treating immunocompromised patients, such as
XX human immunodeficiency virus (HIV) patients, or in improving vaccines.
XX
XX Claim 7; SEQ ID NO 2; 113pp; English.
XX
XX The invention relates to a novel isolated zai1phal1 ligand polypeptide.
XX The polypeptide of the invention may be useful for boosting immunity to
XX infectious diseases and treating immunocompromised patients, such as HIV
XX patients, as well as in improving vaccines. The current sequence is that
XX of the human zai1phal1 ligand protein of the invention.
XX
XX Sequence 162 AA:
XX
XX Query Match 99.3%; Score 706; DB 7; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-73;
XX Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QGODRHMIRKROLIDIVDQKNYVNDIVPEFLPAPBEDVETNCESAFSCFOKQOLKSANT 61
DB 30 QGODRHMIRKROLIDIVDQKNYVNDIVPEFLPAPBEDVETNCESAFSCFOKQOLKSANT 89
QY 62 GNNERIINVSISKLLKRRKPSTNAGRQKHRLTCPSCSYKKPKPEFLERFKSLLOQMIIH 121
DB 90 GNNERIINVSISKLLKRRKPSTNAGRQKHRLTCPSCSYKKPKPEFLERFKSLLOQMIIH 149
QY 122 QHLSRTHGSEDS 134
DB 150 QHLSRTHGSEDS 162

RESULT 13
```

```
ADH10501
ID ADH10501 standard; protein; 162 AA.
XX
XX ADH10501;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human interleukin-21 (IL-21) polypeptide.
XX
XX IL-21; interleukin-21; cytostatic; virucide; antiinflammatory;
XX hepatotropic; neuroprotective; muscular; respiratory; antiarthritic;
XX antibacterial; anti-HIV; gene therapy; cancer; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Key 32..162
XX Peptide /note="specifically claimed fragment"
XX Peptide 41..148
XX /note="specifically claimed fragment"
XX
XX WC2003103589-A2.
XX
XX 18-DEC-2003.
XX
XX 06-JUN-2003; 2003WO-US017808.
XX
XX 07-JUN-2002; 2002US-0387127P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Nelson AJ, Hughes SD, Holly RD, Kindsvogel WR;
XX
XX WPI; 2004-062206/06.
XX
XX N-PSDB; ADH10500.
XX
XX Treating Non-Hodgkin's lymphoma, cancer or infection comprises
XX administering to the subject a polypeptide having a functional activity
XX of interleukin-21.
XX
XX Claim 9; SEQ ID NO 2; 154pp; English.
XX
XX The invention relates to treating Non-Hodgkin's lymphoma, cancer or
XX infection and involves administering to the subject a polypeptide having
XX a functional activity of interleukin-21 (IL-21). The methods are useful
XX for treating Non-Hodgkin's lymphoma; cancer such as renal cell carcinoma,
XX epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and
XX colon cancer; viral infection such as AIDS, Hepatitis B or C virus,
XX gastroenteritis, haemorrhagic diseases, enteritis, cardiac,
XX encephalitis, paralysis, bronchiolitis, upper or lower respiratory
XX disease, respiratory papillomatosis, arthritis, disseminated disease,
XX meningitis, and mononucleosis; or bacterial infection, such as an
XX infection by a bacteria selected from chlamydiae, listeriae, helicobacter
XX pylori, mycobacterium, mycoplasma, salmonella, and shigella, or sudden
XX acute respiratory syndrome caused by a coronavirus, Herpes Simplex
XX viruses, Epstein-Barr virus, Cytomegalovirus, Pox viruses, Papilloma
XX virus, Adenovirus, Poliovirus, Orthomyxoviruses, Paramyxoviruses,
XX Influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses.
XX The present sequence represents a human IL-21 polypeptide.
XX
XX Sequence 162 AA:
XX
XX Query Match 99.3%; Score 706; DB 8; Length 162;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-73;
XX Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 QGODRHMIRKROLIDIVDQKNYVNDIVPEFLPAPBEDVETNCESAFSCFOKQOLKSANT 61
DB 30 QGODRHMIRKROLIDIVDQKNYVNDIVPEFLPAPBEDVETNCESAFSCFOKQOLKSANT 89
QY 62 GNNERIINVSISKLLKRRKPSTNAGRQKHRLTCPSCSYKKPKPEFLERFKSLLOQMIIH 121
DB 90 GNNERIINVSISKLLKRRKPSTNAGRQKHRLTCPSCSYKKPKPEFLERFKSLLOQMIIH 149
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QY	2	QGDPRHMRKQOLIDIVDQKNYNDIVPEPLPAPEVETNCESWAFSCFOKAQKKSANT	61
Db	30	QGDPRHMRKQOLIDIVDQKNYNDIVPEPLPAPEVETNCESWAFSCFOKAQKKSANT	89
QY	62	GNNERTINVSIXKLRKPPSTNAGRQKRLTCDSCSYEKKPPKEPLERFKSLQKMIH	121
Db	90	GNNERTINVSIXKLRKPPSTNAGRQKRLTCDSCSYEKKPPKEPLERFKSLQKMIH	149
QY	122	QHLSSRTHGSEDS	134
Db	150	QHLSSRTHGSEDS	162

Search completed: August 14, 2006, 21:46:36  
Job time : 198 secs

1	94.5	13.3	162	1	A53484
2	91.5	12.9	567	2	S29498
3	82	11.5	607	1	ABXJ72
4	79	11.1	206	2	S49882
5	78	11.0	741	2	JC7822
6	75.5	11.6	336	2	S42632
7	74	10.4	440	2	T47906
8	74	10.4	2197	2	B71600
9	73.5	10.3	162	2	I49124
10	73.5	10.3	472	2	I59087
11	73.5	10.3	868	2	T31527
12	73	10.3	304	2	A32108
13	73	10.3	848	2	T00372
14	72.5	10.2	309	2	T41889
15	72.5	10.2	674	2	S61181
16	72.5	10.2	1101	2	T26919
17	72.5	10.2	1206	2	S24407
18	72	10.1	257	2	C69230
19	72	10.1	262	2	F72858
20	72	10.1	262	2	T41813
21	71.5	10.1	195	2	S42022
22	71.5	10.1	741	2	A83317
23	71	10.0	321	2	T48352
24	71	10.0	406	2	T28857
25	71	10.0	719	2	T27977
26	71	10.0	805	2	A46266
27	71	10.0	864	2	T08575
28	71	10.0	899	2	B38529
29	71	10.0	1231	2	T22382

30	71	10.0	2206	2	G71611	hypothetical protein
31	71	10.0	2324	2	T93878	variant-specific s
32	70.5	9.9	352	2	C86294	T24D18.7 protein -
33	70.5	9.9	477	2	S39316	CAB3b protein - hu
34	70.5	9.9	447	2	S21049	calcium channel pr
35	70.5	9.9	482	2	S41211	voltage-dependent
36	70.5	9.9	484	2	S39315	CAB3a protein - hu
37	70.5	9.9	484	2	A46608	voltage-dependent
38	70.5	9.9	565	2	G88878	conserved hypothet
39	70	9.8	403	2	S71356	glucocorticoid-acti
40	70	9.8	405	2	A79389	senser histidine k
41	70	9.8	425	2	T50355	hypothetical prote
42	70	9.8	1222	2	C88504	protein B0361.3 [1
43	70	9.8	1366	2	B86292	F7H2.12 protein -
44	69.5	9.8	380	2	T25454	hypothetical prote
45	69.5	9.8	864	2	S60441	hypothetical prote

## ALIGNMENTS

```

RESULT 1
A53484
interleukin-15 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A53484
R:Grabstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Bee
I:Gatti, J.G.
Science 264, 965-968, 1994
A>Title: Cloning of a T cell growth factor that interacts with the beta chain of the int
A:Reference number: A53484; MUID:94233380; PMID:8178155
A:Accession: A53484
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-162 <GRA>
A:Cross-references: UNIPROT:P40221; UNIPARC:UPI000003JAC6; GB:U03099; NID:g493521; PIDN:
A>Note: the complete translation is not shown
C:Superfamily: interleukin-15
C:Keywords: growth factor
F:/4-162/Product: interleukin-15 #status predicted <MAT>
F:/83-133,90-136/Dissulfide bonds: #status predicted

Query Match      13.3%; Score 94.5; DB 1; Length 162;
Best Local Similarity 25.9%; Pred.No.0.11; 48; Indels 15; Gaps 5;
Matches 30; Conservative 23; Mismatches

QY      15 IDVDQLKNVNDLVPDF-----LPAPEDVTETCEWSAFSF----OKAOLKSANTGNNE 65
        ::: :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       51 VNVISDLKK-IEDLIQSHIDATLYTESDVHRSCKTAKKCFLELDIVISHESGDTHD 109

QY      66 RIINVSIKKLRRKPSTNAGRQRKHRLTCPSCDSYEKKPKPEFLERFKSLLOKMII 121
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       110 TVEWLLI-LANNILISNGNITES---GCKECEEELKEKNIKERTIQSPVHVLTQWPIN 160

RESULT 2
S29498
lymphocyte antigen Ly94 precursor - mouse
N:Alternate names: 38.5K.T1 glycoprotein; ST2L protein
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S29498; A33541; S176571; S07054
R:Yanagisawa, K.; Takagi, T.; Tsukamoto, T.; Tetuka, T.; Tomimaga, S.
FEBS Lett. 318, 83-87, 1993
A>Title: Presence of a novel primary response gene ST2L, encoding a product highly similar
A:Reference number: S29498; MUID:93170492; PMID:7516701
A:Accession: S29498
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-567 <VAN>
A:Cross-references: UNIPROT:P14719; UNIPARC:UPI0000023617; EMBL:D13695; NID:g286100; PIDN:
R:Klemenz, R.; Hoffmann, S.; Werenkold, A.K.
```

Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989

A/Title: Serum- and oncoprotein-mediated induction of a gene with sequence similarity to A/Reference number: A33541; MUID:89345536; PMID:2527364

A/Accession: A33541

A/Molecule type: mRNA

A/Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <KLE>

A/Cross-references: UNIPARC:UPI0000028A98; GB:M24843; NID:g201103; PIDN:AAA40160.1; PID:R/Tominaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, T.

Biochim. Biophys. Acta 1090, 1-8, 1991

A/Title: Molecular cloning of the murine ST2 gene. Characterization and chromosomal map

A/Reference number: S17657; MUID:91355215; PMID:1832015

A/Accession: S17657

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-191, 'V', 193-328, 'SKECPSHIA' <TOM>

A/Cross-references: UNIPARC:UPI0000028A98; EMBL:X60184; NID:g54200; PIDN:CAA42742.1; PID:R/Tominaga, S.I.

FEBS Lett. 258, 301-304, 1989

A/Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly si

A/Reference number: S07054; MUID:90092495; PMID:2532153

A/Accession: S07054

A/Molecule type: mRNA

A/Residues: 1-328, 'SKECPSHIA' <TO2>

A/Cross-references: UNIPARC:UPI0000003FPD; EMBL:Y07519; NID:g55517; PIDN:CAA68812.1; PID:A/Note: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator

C/Genetics: A/Gene: ST2

A/Map position: 1

A/Intons: 27/1; 97/2; 155/3; 210/1; 233/1; 280/2

C/Superfamily: Interleukin-1 receptor type 1

C/Keywords: glycoprotein

F/1-26/Domain: signal sequence #status predicted <SIG>

F/27-337/Product: ST2 protein #status predicted <MAT>

F/60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 12.9%; Score 91.5; DB 2; Length 567;

Best Local Similarity 25.6%; Pred. No. 0.74;

Matches 33; Conservative 20; Mismatches 39; Indels 37; Gaps 7;

Db 19 DOLKNYNDLVPPELPAPDEVETNCWMSAFSCFOKALTKSANTGNRRINVSIKLKRRK 78

Db 76 DRLK-----FLPRRV-----DSGIYACV-----IRSENL-NKKGVLNVTIHK---K 113

Qy 79 PPSTN-----AGRRQKRLTSPSCDSYEKKRPKEFLERFKSLQKMIHQH----- 123

Db 114 PPSGNIPDYLVMTSVRSDDKNFKITCTPTDLYMTATVQWQKNGKALQDEPRFRAHRSYLF 173

Qy 124 LSSRTGSE 132

Db 174 IDNVTHDE 182

RESULT 3

ABXL72

74K albumin precursor - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004

C/Accession: B41682; S02693; A05288

R/Moskatis, J.E.; Sargent, T.D.; Smith Jr., L.H.; Paetori, R.L.; Schoenberg, D.R.

Mol. Endocrinol. 3, 464-473, 1989

A/Title: Xenopus laevis serum albumin: sequence of the complementary deoxyribonucleic ac e during development.

A/Reference number: A41682; MUID:99313788; PMID:2747653

A/Accession: B41682

A/Molecule type: mRNA

A/Residues: 3-607 <MOS>

A/Cross-references: UNIPROT:P14872; UNIPARC:UPI00001714FB; GB:M21442; NID:g213930; PIDN:R/Schorpp, M.; Doebbeling, U.; Wagner, U.; Ryffel, G.U.

J. Mol. Biol. 199, 83-93, 1988

A/Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. Delc

A/Reference number: S02692; MUID:88172470; PMID:2451026

A/Accession: S02693

A/Status: not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-48 <SCH>

A/Cross-references: UNIPARC:UPI000017441E; EMBL:Z26826

R/Molfe, A.P.; Glover, J.F.; Martin, S.C.; Tenniwood, M.P.R.; Williams, J.L.; Tata, J.J

Eur. J. Biochem. 146, 489-496, 1985

A/Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and deestabilizator

A/Reference number: A05288; MUID:85126974; PMID:3971963

A/Accession: A05288

A/Molecule type: mRNA

A/Residues: 459-502, 'L', 504-557 <WOL>

A/Cross-references: UNIPARC:UPI000017441F; GB:M28276

A/Note: the authors translated the codon TAT for residue 63 as Thr

C/Comment: Serum albumin is synthesized in the liver as prealbumin. It binds copper, i mones (weak bonds with these hormones promote their transfer across the membranes), thyrc

C/Genetics: A/Intons: 27/1

C/Superfamily: serum albumin; serum albumin repeat homology

C/Keywords: carrier protein; duplication; glycoprotein; metal binding; plasma

F/1-18/Domain: signal sequence #status predicted <SIG>

F/19-24/Domain: propeptide #status predicted <PRO>

F/25-607/Product: 74K serum albumin #status predicted <MAT>

F/32-201/Domain: serum albumin repeat homology <SA1>

F/220-393/Domain: serum albumin repeat homology <SA2>

F/442-591/Domain: serum albumin repeat homology <SA3>

F/30/Binding site: copper (His) #status predicted

F/80-88,101-117,116-127,147-191-200,223-265,268-276,288-302,301-312,339-384,383-392,4 F/256/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.5%; Score 82; DB 1; Length 607;

Best Local Similarity 24.2%; Pred. No. 6.3;

Matches 38; Conservative 19; Mismatches 50; Indels 50; Gaps 6;

Qy 16 DIVDOLKNYNDLVPPELPAPDEVETNCWMSAFSCF-----QKALTKSAN 60

Db 72 EINDPAKSCINDTPBECKVGTLPFDKLCADPAVGNTVMSKCAKQDPKAAQCFKAAH 131

Qy 61 TGNNERIT---NVSIKCLKRK-----PPSTNAGRQKRLTSPS 96

Db 132 RDHEHTSIKPEPEETGTLKEHPDDLAFIHEARNHPDLPVAVLATKYHKLAEHC 191

Qy 97 CDSYEKKRPKEFLERFKSLQKMIHQHLSRTGSHD 133

Db 192 CEEEDKE--KCFSEKMKQLMK-----QSHSID 217

RESULT 4

S49882

hypothetical protein Y1127c - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein Y18277.Ozc

C/Species: Saccharomyces cerevisiae

C/Date: 13-Jan-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C/Accession: S49882

R/Hamlyn, N.; Churcher, C.

submitted to the EMBL Data Library, November 1994

A/Reference number: S49882

A/Accession: S49882

A/Molecule type: DNA

A/Residues: 1-206 <HAM>

A/Cross-references: UNIPROT:P40470; UNIPARC:UPI000013B441; GB:Z47047; EMBL:Z46833; NID:9C

C/Genetics: A/Gene: MIPS:Y1127c

A/Cross-references: SGD:S0001389

A/Map position: 9L

Query Match 11.1%; Score 79; DB 2; Length 206;

Best Local Similarity 26.1%; Pred. No. 3.9;

Matches 29; Conservative 18; Mismatches 48; Indels 16; Gaps 3;

Qy 20 QLKNYNDLVPPELPAPDEVETNCWMSAFSCFOKALTKSANTGNRRINVSIKLKRRK 79

Db 12 QATSVANGLSNLPLPGVFKIRANGKTSVANGSKAQLIDNLKKRQVLQQRVDYHKKKCC 71

Qy 80 PSTNAGRQKRLTSPSCDSYEKKRPKEFLERF--KSLQKMIHQHLSRT 128



Db 72 KLVRKKVKVKKHKL-----DKKQLAKHGVLLKK--HQHGGTLT 108

## RESULT 5

JC7822  
Isocitrate dehydrogenase (NADP) (EC 1.1.1.42), monomeric type - Azotobacter vinelandii

C/Species: Azotobacter vinelandii  
C/Date: 03-Jun-2002 #sequence\_revision 03-Jun-2002 #text\_change 09-Jul-2004

C/Accession: JC7822; PC7187

R/Sahara, T.; Takada, Y.; Takeuchi, Y.; Yamaoka, N.; Fukunaga, N.

Biosci. Biotechnol. Biochem. 66, 489-500, 2002

A/Title: Cloning, sequencing, and expression of a gene encoding the monomeric isocitrate

A/Reference number: JC7822; PMID:12005040; PMID:21999801

A/Accession: JC7822

A/Molecule type: DNA

A/Residues: 1-741 <SAH>

A/Cross-references: UNIPROT:P16100; UNIPARC:UPI000012D1CA; DDBJ:D73443

A/Accession: PC7187

A/Molecule type: protein

A/Residues: 2-16 <SA>

A/Cross-references: UNIPARC:UPI0000176DF5

C/Comment: This enzyme that catalyzes the oxidative decarboxylation of isocitrate to alpha

his bacterium is typical mesophilic, it contributes to the respiratory protection of nit

C/Genetics:

A/Gene: 1cd

C/Superfamily: isocitrate dehydrogenase, monomeric type

C/Keywords: oxidoreductase

Query Match 11.0%; Score 78; DB 2; Length 741;  
Best Local Similarity 24.8%; Pred. No. 18;

Matches 26; Conservative 23; Mismatches 34; Indels 22; Gaps 4;

Db 5 DRHMIRBQIDIVDQKNVNDL-----VPEFLPAPEDVTNCESAFSCFOKAOLKS 58

Db 77 DANITKLPNISASVPQKALIKELQOGGYKLPDY--PEEKTDTEDVAKRDKIKGSA 133

Db 59 AN-----TGNRRITNVSIKKLKKRPPSTNAGRQKRLTSPSCDS 99

Db 134 VNVVLRGNSDRAPLSVKYARKRP-----HKGMSADS 169

## RESULT 6

S42632  
F1t-15 protein precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 25-Dec-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C/Accession: S42632

R/Bergers, G.; Reikertorfer, A.; Braedelmann, S.; Graninger, P.; Bueslinger, M.

EMBO J. 13, 1176-1180, 1994

A/Title: Alternative promoter usage of the Fos-responsive gene F1t-1 generates mRNA isofo

A/Reference number: S42632; PMID:94178260; PMID:8131748

A/Accession: S42632

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-336 <BBR>

A/Cross-references: UNIPROT:Q62611; UNIPARC:UPI000002AC15; GB:U04319; NID:9488278; PIDN:

C/Superfamily: vaccinia virus B15R protein; immunoglobulin homology

Query Match 10.6%; Score 75.5; DB 2; Length 336;  
Best Local Similarity 22.2%; Pred. No. 14;

Matches 30; Conservative 26; Mismatches 42; Indels 37; Gaps 6;

Db 15 IDIVDQKNVNDLVP-----EFLPAPEDVTNCESAFSCFOKAOLKSAN 60

Db 49 INVENVYSWTNRIPIQKRNRIIVSHDRKLPAPKE-----DSGYTCVIRSP-ESIK 102

Db 61 TGNRRITNVSIKKLKKRPP-----STNAGRQKRLTSPSCDSYEKKPPKFELE 110

Db 103 TGS-----LWTLTK--RPENCKIPDYMTSTVDGSDKSKITPTALTATWTAAPVGMFK 155

Db 111 RFSLLQKMTIHOLS 125

Db 111 RFSLLQKMTIHOLS 125

Db 156 NCKALQGPFRFAMS 170

## RESULT 7

T47906  
FUSCA PROTEIN FUS6 - Arabidopsis thaliana

N/Alternate names: protein T20K12.40

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 05-Oct-2004

C/Accession: T47906

R/De Haan, M.; Maarre, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Meyer, K.F.X.; Queti

submitted to the Protein Sequence Database, January 2000

A/Reference number: 224480

A/Accession: T47906

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-440 <DEH>

A/Cross-references: UNIPROT:P45432; UNIPARC:UPI000016DBFF; EMBL:AL137898

A/Experimental source: cultivar Columbia; BAC clone T20K12

C/Genetics:

A/Map position: 3

A/Introns: 130/3; 237/3; 278/1; 304/2; 382/3

A/Note: T20K12.40

C/Superfamily: COP9 signalosome complex subunit 1

Query Match 10.4%; Score 74; DB 2; Length 440;  
Best Local Similarity 22.0%; Pred. No. 25;

Matches 26; Conservative 22; Mismatches 50; Indels 20; Gaps 3;

Db 6 RHMIRBQIDIVDQKNVNDLVPPEFLPAPEDVTNCESAFSCFOKAOLKSANTGNE 65

Db 230 KYKLAARKFLVDNBLGNSVNEVI-----APQDIATVGGICALASFRSEIKAF----- 278

Db 66 RIINVSIKKLKKRPPSTNAGRQKRLTSPSCDSYEKKPPPEFLERKSLQKMTIHCH 123

Db 279 -IDNINFRNLELVDPVRELINDPSSRYASC-----LEVLASIKSLNLLDIIHLH 327

## RESULT 8

B71600  
variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium falciparum)

N/Alternate names: erythrocyte membrane binding protein 1 (EMPI1)

C/Species: Plasmodium falciparum

C/Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 09-Jul-2004

C/Accession: B71600

R/Gardner, M.J.; Tetteilin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

Science 282, 1126-1132, 1998

A/Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A/Reference number: A71600; PMID:99021743; PMID:9804551

A/Accession: B71600

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-2197 <GAR>

A/Cross-references: UNIPROT:Q96296; UNIPARC:UPI00001796B2; GB:AE001434; GB:AE001362; NID:

A/Experimental source: clone 307

C/Genetics:

A/Gene: PFB1055c

Query Match 10.4%; Score 74; DB 2; Length 2197;  
Best Local Similarity 29.5%; Pred. No. 1,4e+02;

Matches 28; Conservative 16; Mismatches 41; Indels 10; Gaps 4;

Db 21 LKATVNDLVPPEFLPAPEDVTNCESAF--SCFOKAOLKSANTGNRRITNVSIKKLKK 78

Db 1594 VKSFLETWIPK-IAVVDQDNVTKLSFKGNSCGCSAISTN-GNEBDALDCMTKLEKK 1651

Db 79 -----PSTNAGRQKRLTSPSCDSYEKKPPK 107

Db 1652 IDECKRFGNSGTCNMTLTHPLDVODEDEPLEE 1686

Db 1652 IDECKRFGNSGTCNMTLTHPLDVODEDEPLEE 1686

## RESULT 9

[illegible]

```

C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31527
R:Matthews, L.
submitted to the EMBL Data Library, October 1999
A:Reference number: Z21043
A:Accession: T31527
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-868 <MW>
A:Cross-references: UNIPROT:Q9NNAH8; UNIPARC:UPI0000179F16; EMBL:AL117202; PIDN:CAE55073.1
A:Experimental source: clone Y47D3A
C:Genetics:
A:Gene: CESP:Y47D3A.14
A:Introns: 17/2, 51/3; 102/3; 169/3; 246/1; 287/2; 319/3; 371/3; 395/2; 440/3; 450/3; 495/2
Query Match      10.3%; Score 73.5; DB 2; Length 866;
Best Local Similarity 29.2%; Pred. No. 57;
Matches 19; Conservative 11; Mismatches 30; Indels 5; Gaps 1;

Cy      45 WSASFCEPQAOLKS-----ANTGNNERTIIVNSIKKILKKRPSTINAGRKORLTCPSCDS 99
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      680 WSRVQAFRRKNMKGSGGGGTNSDDSSQBSBKVLKKLKARRPSDETVLPVPHYTCPLFFS 739
          ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Cy      100 YEKP 104
           |
Db      740 HVATP 744

RESULT 12
A32108
translation initiation factor eIF-2 alpha chain - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein J1429; protein YOR007w
C:Species: Saccharomyces cerevisiae
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A32108; S55195; S57022
R:Cigan, A.M.; Pabich, E.K.; Feng, L.; Donahue, T.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 2784-2788, 1989
A>Title: Yeast translation initiation suppressor suiz2 encodes the alpha-subunit of eukaryotic
A:Reference number: A32108; MUID:89202411; PMID:2649894
A:Accession: A32108
A:Molecule type: DNA
A:Residues: 1-304 <Clg>
A:Cross-references: UNIPROT:P20459; UNIPARC:UPI00000530CA; EMBL:M25552; NID:g341369; PIDN:
R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A:Reference number: S55183
A:Accession: S55195
A:Molecule type: DNA
A:Residues: 1-304 <DH>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:X67611; NID:g854567; PIDN:CAA60929.1; PI
R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56771
A:Accession: S57022
A:Molecule type: DNA
A:Residues: 1-304 <ZAG>
A:Cross-references: UNIPARC:UPI00000530CA; EMBL:z49507; NID:g1015631; PIDN:CAA89529.1; PI
C:Genetics:
A:Gene: SGD:SUI2
A:Cross-references: SGD:S0003767; MIPS:YJR007w
A:Map position: 10R
C:Superfamily: translation initiation factor eIF-2 alpha chain
C:Keywords: phosphoprotein; protein biosynthesis

Query Match      10.3%; Score 73; DB 2; Length 304;
Best Local Similarity 24.8%; Pred. No. 21;
Matches 34; Conservative 25; Mismatches 56; Indels 22; Gaps 7;

Cy      16 DIVDLTKNYVD-LVPEFLPAPEDEVETNC-EWSAFSCFOKAOLKSANTGNNERI-INVISI 72
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      164 DVLDLTKNYISRLTPQAVKIADVEVSCFSYRGIDAIKDA-LKSAEDMSSTEGWGVAKTL 222

```

Qy 73 KKLKRPSTNAGRQKRLTCPSCDSEYK-----KPKPELRFKSLIQ 117  
 Db 223 VAAPLVLTQALQKQKIQEQLS--ALEKITVITKYGVGNITMPKAVTATEDALQ 280  
 Qy 118 KMH-QHLSRTHGSED 133  
 Db 281 ALLESKELDNRSDEDD 297

## RESULT 13

T00372  
 hypothetical protein KIAA0650 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004

C/Accession: T00372; T12523

R/Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.

DNA Ref. 5, 169-176, 1998

A/Title: Prediction of the coding sequences of unidentified human genes. X. The complete

A/Reference number: Z14142; MUID:98403880; PMID:9734811

A/Accession: T00372

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-848 <ISH>

A/Cross-references: UNIPROT:O75141; UNIPARC:UPI000006CEB7; EMBL:AB014550; NID:G3327113;

A/Experimental source: brain

R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

A/Reference number: Z17524

A/Accession: T12523

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-122-848 <WAM>

A/Cross-references: UNIPARC:UPI0000072B1E; EMBL:AL080138

A/Experimental source: adult testis; clone DKFZp434K063

C/Genetics:

A/Note: KIAA0650; DKFZp434K063.1

Query Match 10.3%; Score 73; DB 2; Length 848;  
 Best Local Similarity 25.5%; Pred. No. 62;  
 Matches 27; Conservative 22; Mismatches 47; Indels 10; Gaps 5;  
 Qy 31 EFLPAPEDVETNC-EMSAFSCFOQAOLKSANTGNNERIINVSIRKLKRPSTNAGRQK 89  
 Db 66 KFLRPGPNNDLCTWBEFSDFLRVQLIS--GPPAKLLIDWPELKSIVIN-GRDLQ 121  
 Qy 90 HRLTSPCDSEYKPPKPEFLERFKSLQKMHQL--SSRTHGSED 133  
 Db 122 NPILVQLCDQMDNPAF--VQHVKISLTKASNLKLMPSNQCHKTDE 164

## RESULT 14

T41889  
 PE38 orf153 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C/Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV

A/Variety: isolate T3

C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C/Accession: T41889

R/Gomi, S.; Majima, K.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999

A/Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A/Reference number: Z22020; MUID:99281911; PMID:10355780

A/Accession: T41889

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-309 <KAM>

A/Cross-references: UNIPROT:O92504; UNIPARC:UPI00000F20C2; EMBL:L33180; NID:G3745835; PI

C/Genetics:

A/Note: pe38

C/Superfamily: Orgyia pseudotsugata nuclear polyhedrosis virus PE-38 protein

Query Match 10.2%; Score 72.5; DB 2; Length 309;  
 Best Local Similarity 23.4%; Pred. No. 24;

Matches 33; Conservative 30; Mismatches 57; Indels 21; Gaps 6;  
 Qy 10 RMROLIDIVDQKRYVNDLVEFLPAPEDVETNC-----EMSAFSCFOQAOLKSAN----- 60  
 Db 148 KQGRVAVQGYKQIIKVLQGRSVISVENSNNCDINNENAKIYALAEALKNEGNHSDQ 207  
 Qy 61 -TGNNERII-----NVSIRKLKRPSTNAGRQKRLTCPSCDSEYKPPKPEFLERFK 113  
 Db 208 VTSENROLIBENTRLNQQVQLQRO-VRTLAPQR---GITVNPQLGRDDRAPAEINERFR 263  
 Qy 114 SLQKMHQ-HLSRTHGSED 133  
 Db 264 SLVYSTISELFEINRVHISION 284

## RESULT 15

S61181  
 hypothetical protein YDR295C - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein D9740.10

C/Species: Saccharomyces cerevisiae

C/Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C/Accession: S61181

R/Ding, H.

submitted to the EMBL Data Library, June 1995

A/Description: The sequence of S. cerevisiae cosmid 9740.

A/Reference number: S61160

A/Accession: S61181

A/Molecule type: DNA

A/Residues: 1-674 <DIN>

A/Cross-references: UNIPROT:Q06629; UNIPARC:UPI00000531D0; EMBL:U28374; NID:9849207; PID:

C/Genetics:

A/Status: SGD:YDR295C

A/Cross-references: SGD:S0002703

A/Map position: 4R

Query Match 10.2%; Score 72.5; DB 2; Length 674;  
 Best Local Similarity 20.0%; Pred. No. 55;  
 Matches 30; Conservative 30; Mismatches 55; Indels 35; Gaps 4;  
 Qy 1 MQGDDRMIMIRROLID-----IVDQKRYVNDLVEFLPAPEDV 39  
 Db 495 LQNKINHLKKNROELNENFNKLPSNTISSENLREGSALADLKAYIDKNATLFNKLKELQ 554  
 Qy 40 ETNCEWGAFA-----SCFOQAOLKSANTGNNERIINVSIRKLKRP-----STNAGRQ 88  
 Db 555 QANAEKKNLDELRSKQIIESSKAAESAOYIKILQESMKSLENEVNGPLTKFTESLAKGE 614  
 Qy 89 KHLTSPCDSEYKPPKPEFLERFKSLQK 118  
 Db 615 LERL---QNDPQSLKARNKFLKNVITLMNR 641

Search completed: August 14, 2006, 21:52:27  
 Job time : 42 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2006, 21:43:28 ; Search time 301 Seconds  
(without alignments)

411.801 Million cell updates/sec

Title: US-10-735-149-28

Perfect score: 711

Sequence: 1 MQQDMMIRMLRLIDIVDQ.....LLQKMHQHLSTRTHGSEDS 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	706	99.3	155 1 IL21_HUMAN	Q9B642 homo sapien
2	535	75.2	146 1 IL21_BOVIN	Q76145 bos taurus
3	524	73.7	146 1 IL21_PIG	Q76145 sus scrofa
4	513	72.2	146 1 IL21_CANIS	Q61719 canis famul
5	404	56.8	146 1 IL21_MOUSE	Q95171 mus musculu
6	404	56.8	146 1 IL21_MOUSE	Q95171 mus musculu
7	344	48.4	123 1 IL21_PERNA	Q80XG2 peromyscus
8	149.5	21.0	145 2 IL21_CHICK	Q58166 gallus gall
9	101.5	14.3	162 1 IL15_FELICA	Q97687 felis silve
10	99.5	14.0	135 2 Q6FGX7_HUMAN	Q6FGX7 homo sapien
11	99.5	14.0	162 1 IL15_HUMAN	Q40933 homo sapien
12	99.5	14.0	162 2 Q49528_HUMAN	Q49528 homo sapien
13	98.5	13.9	162 1 IL15_RABIT	Q3Y5G8 oryctolagus
14	96.5	13.6	162 1 Q5W7F5_BRARE	Q5W7F5 brachydanio
15	94.5	13.3	160 2 Q32PM5_BRARE	Q32PM5 brachydanio
16	94.5	13.3	162 1 IL15_CERAE	P40221 cercopithec
17	94.5	13.3	162 1 IL15_MACACA	Q48092 macaca mula
18	94.5	13.3	162 2 Q4U0U2_MACTH	Q4U0U2 macaca thib
19	93.5	13.2	145 2 Q38121_TETNG	Q38121 tetradon n
20	92	12.9	163 2 Q2PUG6_RABIT	Q2PUG6 oryctolagus
21	91.5	12.9	337 2 Q5D095_MOUSE	Q5D095 mus musculu
22	91.5	12.9	567 1 IL15_MOUSE	P14719 mus musculu
23	91.5	12.9	567 1 Q3UM53_MOUSE	Q3UM53 mus musculu
24	90.5	12.7	162 1 IL15_BOVIN	Q28028 bos taurus
25	89.5	12.6	162 1 IL15_SHEEP	Q9X916 ovis aries
26	89.5	12.6	162 2 Q75529_CAVPO	Q75529 cavia porce
27	87.5	12.3	162 2 Q6B416_HORSE	Q6B416 equus cabal
28	85.5	12.0	105 2 Q5W7F6_BRARE	Q5W7F6 brachydanio
29	85.5	12.0	162 2 Q4GZ11_BUBBU	Q4GZ11 brachydanio
30	85	12.0	162 2 Q5E8K6_MARMO	Q5E8K6 marmota mon
31	85	12.0	162 2 Q5WQV8_MARMO	Q5WQV8 marmota mon

32	84.5	11.9	511 2 Q5A2U1_CANAL	Q5A2U1 candida alb
33	83.5	11.7	466 2 Q5C0J3_SCHUA	Q5C0J3 schistosoma
34	83.5	11.7	582 2 Q8DJ56_SYNEL	Q8DJ56 synechococ
35	83.5	11.7	3052 2 Q82933_9PORTV	Q82933 johnsongras
36	83	11.7	607 2 Q642P7_XENLA	Q642P7 xenopus lae
37	82.5	11.6	149 2 Q59A52_FUGRU	Q59A52 figu rubrip
38	82	11.5	607 1 ALBUD_XENLA	P14872 xenopus lae
39	81.5	11.5	566 2 Q9VYE8_DROME	Q9VYE8 drosophila
40	81	11.4	163 2 Q966R0_DICDI	Q966R0 dictyosteli
41	81	11.4	414 2 Q7MNL4_VIBVY	Q7MNL4 vibrio vuln
42	81	11.4	1111 2 Q6FKR1_CANCA	Q6FKR1 candida gla
43	80.5	11.3	155 2 Q59902_FUGRU	Q59902 figu rubrip
44	80.5	11.3	162 1 IL15_PIG	Q95253 sus scrofa
45	80.5	11.3	353 2 Q2UGB6_ASFOR	Q2UGB6 aspergillus

## ALIGNMENTS

RESULT 1	ID	IL21_HUMAN	STANDARD	PRT: 155 AA.
AC	Q9HBE4	23-NOV-2004, integrated into UniProtKB/Swiss-Prot.		
DT	23-NOV-2004, integrated into UniProtKB/Swiss-Prot.			
DT	07-FEB-2006, entry version 24.			
DE	Interleukin-21 precursor (IL-21) (Zal1).			
GN	Name=IL21;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.			
RX	MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;			
RA	Parish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C., Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S., Burkhead S., Heipel M., Brandt C., Knipper J.L., Kramer J., Conklin D., Presnell S.R., Berry J., Shota F., Bort S., Handly K., Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T., Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T., Maurer M., Kaushansky K., Holly R.D., Foster D.; "Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function."; Nature 408:57-63 (2000).			
RL	[2]			
RA	Nguyen D.A., Livingston J., Posl C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Mitrak L.A., Nickerson D.A.; "SeattlesNP, NHLBI H66682 program for genomic applications, UW-FORC, Seattle, WA (URL: http://pga.gs.washington.edu)"; submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).			
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straubenberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Bock S.S., Loquellano N.A., Peters G.J., Abramson J., Mullaly S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultay S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting J., Madan A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP FUNCTION:  
 RX PubMed=15178704; DOI=10.1189/jlb.1003488;  
 RX Stenegren M., Julkunen I., Matikainen S.;  
 RT "IFN-alpha regulates IL-21 and IL-21R expression in human NK and T  
 RT cells.";  
 RL J. Leukoc. Biol. 76:416-422(2004).  
 RN [5]  
 RP REVIEW.  
 RX PubMed=15147560; DOI=10.1111/j.1365-2567.2004.01886.x;  
 RX Sivakumar P.V., Foster D.C., Clegg C.H.;  
 RA "Interleukin-21 is a T-helper cytokine that regulates humoral immunity  
 RT and cell-mediated anti-tumour responses.";  
 RL Immunology 112:177-182(2004).  
 CC -I- FUNCTION: Cytokine with immunoregulatory activity. May promote the  
 CC production of IgG(1) and IgG(3) in B-cells (By similarity). May  
 CC play a role in proliferation and maturation of natural killer (NK)  
 CC cells in synergy with IL15. May regulate proliferation of mature  
 CC B- and T-cells in response to activating stimuli. In synergy with  
 CC IL15 and IL18 stimulates interferon gamma production in T-cells  
 CC and NK cells. During T-cell mediated immune response may inhibit  
 CC dendritic cells (DC) activation and maturation.  
 CC -I- SUBCELLULAR LOCATION: Secreted protein.  
 CC -I- TISSUE SPECIFICITY: Expressed in activated CD4-positive T-cells  
 CC but not in CD8-positive T-cells, B-cells, or monocytes.  
 CC -I- SIMILARITY: Belongs to the IL-21 family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivative License  
 CC -----  
 CC EMBL: AF254069; AAC29348.1; ALT\_INIT; mRNA.  
 CC EMBL: AY763518; AA088182.1; ALT\_INIT; Genomic\_DNA.  
 CC EMBL: BC066258; AA066258.1; ALT\_INIT; mRNA.  
 CC EMBL: BC066259; AA066259.1; ALT\_INIT; mRNA.  
 CC EMBL: BC066260; AA066260.1; ALT\_INIT; mRNA.  
 CC EMBL: BC066261; AA066261.1; ALT\_INIT; mRNA.  
 CC EMBL: BC066262; AA066262.1; ALT\_INIT; mRNA.  
 CC EMBL: BC069124; AA069124.1; ALT\_INIT; mRNA.  
 CC EMBL: ENSG00000138684; Homo sapiens.  
 CC HGNC: HGNC:6005; IL21.  
 CC MIM: 605384; gene.  
 CC DR GO: GO:0005615; C:extracellular space; NAS.  
 CC DR GO: GO:0005134; F:interleukin-2 receptor binding; IPI.  
 CC DR GO: GO:0048469; P:cell maturation; IDA.  
 CC DR GO: GO:0045078; P:positive regulation of interferon-gamma bio. .; NAS.  
 CC DR GO: GO:0042102; P:positive regulation of T cell proliferation; IDA.  
 CC DR GO: GO:0007165; P:signal transduction; NAS.  
 CC CYTOKINE; Glycoprotein; Signal.  
 CC KW CHAIN 1 22 Potential.  
 CC FT SIGNAL 23 155 Interleukin-21.  
 CC FT CARBOHYD 90 90 N-linked (GlcNAc... ) (Potential).  
 CC FT DISULFID 64 115 Potential.  
 CC FT DISULFID 71 118 Potential.  
 CC SQ SEQUENCE 155 AA; 17923 MW; B994A3D1902B914 CRC64;  
 QY Query Match 99.3%; Score 706; DB 1; Length 155;  
 QY Best Local Similarity 100.0%; Pred. No. 5,1e-57;  
 QY Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 2 QGDRHMRKRLIDIVDQKNVNDLVPEFLPAPBVDVTNCMSAFCFOKQKLSANT 61  
 DB 23 QGDRHMRKRLIDIVDQKNVNDLVPEFLPAPBVDVTNCMSAFCFOKQKLSANT 82  
 QY GNNRIINVSICKLKRKRPSTNAGROKHLTCSGCSYKPKPEFLERFKSLIQKIH 121  
 QY 62 GNNRIINVSICKLKRKRPSTNAGROKHLTCSGCSYKPKPEFLERFKSLIQKIH 121  
 DB 83 GNNRIINVSICKLKRKRPSTNAGROKHLTCSGCSYKPKPEFLERFKSLIQKIH 142

QY 122 QHLSRTHGSEDS 134  
 DB 143 QHLSRTHGSEDS 155  
 RESULT 2  
 IL21 BOVIN  
 ID IL21 BOVIN STANDARD; PRT; 146 AA.  
 AC 076LDS;  
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 23-NOV-2004, sequence version 2.  
 DT 07-FEB-2006, entry version 12.  
 DE Interleukin-21 precursor (IL-21).  
 GN Name=IL21;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 OC Pecora; Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP NCBIOTIDE SEQUENCE (MRNA), PROTEIN SEQUENCE OF 18-32, SUBCELLULAR  
 RP LOCATION AND TISSUE SPECIFICITY.  
 RX PubMed=12969638; DOI=10.1016/S0165-2427(03)00106-5;  
 RA Muneta Y., Kikuma R., Yoshitara K., Mori Y.;  
 RT "Cloning, expression, and tissue distribution of bovine interleukin-  
 RT 21.";  
 RL Vet. Immunol. Immunopathol. 95:73-80(2003).  
 CC -I- FUNCTION: Cytokine with immunoregulatory activity. May promote the  
 CC transition between innate and adaptive immunity. Induces the  
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in  
 CC proliferation and maturation of natural killer (NK) cells in  
 CC synergy with IL15. May regulate proliferation of mature B- and T-  
 CC cells in response to activating stimuli. In synergy with IL15 and  
 CC IL18 stimulates interferon gamma production in T-cells and NK  
 CC cells (By similarity). During T-cell mediated immune response may  
 CC inhibit dendritic cells (DC) activation and maturation (By  
 CC similarity).  
 CC -I- SUBCELLULAR LOCATION: Secreted protein.  
 CC -I- TISSUE SPECIFICITY: Expressed in spleen, but not in the brain,  
 CC heart, kidney, liver, and lung.  
 CC -I- SIMILARITY: Belongs to the IL-21 family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivative License  
 CC -----  
 CC EMBL: AB073021; BAC87747.1; ALT\_INIT; mRNA.  
 CC CYTOKINE; Direct protein sequencing; Signal.  
 CC KW CHAIN 1 17 Probable.  
 CC FT SIGNAL 18 146 Interleukin-21.  
 CC FT DISULFID 64 115 Potential.  
 CC FT DISULFID 71 118 Potential.  
 CC SQ SEQUENCE 146 AA; 16948 MW; 696566DA73F4B8BC CRC64;  
 QY Query Match 75.2%; Score 535; DB 1; Length 146;  
 QY Best Local Similarity 80.6%; Pred. No. 2.7e-41;  
 QY Matches 100; Conservative 11; Mismatches 13; Indels 0; Gaps 0;  
 DB 2 QGDRHMRKRLIDIVDQKNVNDLVPEFLPAPBVDVTNCMSAFCFOKQKLSANT 61  
 DB 23 QGDRHMRKRLIDIVDQKNVNDLVPEFLPAPBVDVTNCMSAFCFOKQKLSANT 82  
 QY GNNRIINVSICKLKRKRPSTNAGROKHLTCSGCSYKPKPEFLERFKSLIQKIH 121  
 QY 62 GNNRIINVSICKLKRKRPSTNAGROKHLTCSGCSYKPKPEFLERFKSLIQKIH 121  
 DB 83 GNNRIINVSICKLKRKRPSTNAGROKHLTCSGCSYKPKPEFLERFKSLIQKIH 142  
 QY 122 QHLS 125  
 DB 143 QHLS 146  
 RESULT 3

ID	IL21_PIG	STANDARD;	PRT;	146 AA.
AC	Q76U06;			
DT	23-NOV-2004,	integrated into UniProtKB/Swiss-Prot.		
DT	23-NOV-2004,	sequence version 2.		
DT	07-FEB-2006,	entry version 12.		
DE	Interleukin-21 precursor (IL-21).			
GN	Name=IL21;			
OS	Sus scrofa (pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;			
OC	Su.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [mRNA], FUNCTION, AND SUBCELLULAR LOCATION.			
RX	PubMed:15107555; DOI=10.1292/jvms.66.269;			
RA	Muneta Y., Kikuma R., Uenishi H., Hoshino T., Yoshihara K., Tanaka M.,			
RA	Hamashima N., Mori Y.;			
RT	"Molecular cloning, expression and biological function of porcine interleukin-21."			
RL	J. Vet. Med. Sci. 66:269-275(2004).			
CC	-1- FUNCTION: Cytokine with immunoregulatory activity. May promote the transition between innate and adaptive immunity. Induces the production of IgG(1) and IgG(3) in B-cells. May play a role in proliferation and maturation of natural killer (NK) cells in synergy with IL15. May regulate proliferation of mature B- and T-cells in response to activating stimuli. In synergy with IL15 and IL18 stimulates interferon gamma production in T-cells and NK cells (By similarity). During T-cell mediated immune response may inhibit dendritic cells (DC) activation and maturation.			
CC	-1- SUBCELLULAR LOCATION: Secreted protein.			
CC	-1- SIMILARITY: Belongs to the IL-21 family.			
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>			
CC	Distributed under the Creative Commons Attribution-NonCommercial license			
DR	EMBL, AB073020, BAD11128.1, ALU_INIT; mRNA.			
KW	Cytokine; Signal.			
FT	SIGNAL	1	17	Potential.
FT	CHAIN	18	146	Interleukin-21.
FT	DISULFID	64	115	/FTID=PRO_0000015508.
FT	DISULFID	71	118	Potential.
SO	SEQUENCE	146 AA;	16833 MW;	835C63B716230BD1 CRC64;
	Query Match	73.7%;	Score 524;	DB 1; Length 146;
	Best Local Similarity	80.6%;	Pred. No. 2,8e-40;	
	Matches 100;	Conservative 11;	Mismatches 13;	Indels 0; Gaps 0;
QY	2	QGQDRHMIKMEQLIDIVDQIAKRYVNDLVPELPAPEDVETNCWMSAFSCFOKAOLKSNANT	61	
DB	23	QGQDRLLIRLQQLIDTVQIAKRYVHDLPELPAPEDVGRHCEGSAFCFOKVELKSNANT	82	
QY	62	GNMERIIVNSIKKLKKRPPSTNAGRGQRKLTCPSGDYSYKKPPSEPIERRFKSLQIKIHI	121	
DB	83	GDNEKIVIVLKKLKKRKLPTNAGRGQRGLTCPTDYSYKKPIKEPIERLKSILQIKIHI	142	
QY	122	QHLS 125		
DB	143	QHLS 146		
RESULT 4				
ID	IL21_CANPA	STANDARD;	PRT;	146 AA.
AC	Q6L7I9;			
DT	23-NOV-2004,	integrated into UniProtKB/Swiss-Prot.		
DT	05-JUL-2004,	sequence version 1.		
DT	07-FEB-2006,	entry version 11.		
DE	Interleukin-21 precursor (IL-21).			
GN	Name=IL21;			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

CC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 CC Canis.  
 CC NCBI\_TaxID=9615;  
 RN [1]  
 RN NCBIOTIDE SEQUENCE [mRNA].  
 RP TISSUE= spleen.  
 RA Miyake M., Saze K., Haga Y., Yamamoto Y., Iwabuchi S.,  
 RT "Molecular cloning of canine interleukin-21 cDNA.";  
 RL Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.  
 CC CC -1- FUNCTION: Cytokine with immunoregulatory activity. May promote the  
 CC CC transition between innate and adaptive immunity. Induces the  
 CC CC production of Igg(1) and Igg(3) in B-cells. May play a role in  
 CC CC proliferation and maturation of natural killer (NK) cells in  
 CC CC synergy with IL15. May regulate proliferation of mature B- and T-  
 CC CC cells in response to activating stimuli. In synergy with IL15 and  
 CC CC IL18 stimulates interferon gamma production in T-cells and NK  
 CC CC cells (By similarity). During T-cell mediated immune response may  
 CC CC inhibit dendritic cells (DC) activation and maturation (By  
 CC CC similarity).  
 CC CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).  
 CC CC -1- SIMILARITY: Belongs to the IL-21 family.  
 CC CC  
 CC CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC CC Distributed under the Creative Commons Attribution-NoDerivs license  
 CC CC  
 CC EMBL, AB127975, BAD22569.1; -, mRNA.  
 DR Ensemble; ENSGACFG0000004004; Canis familiaris.  
 KW Cytokine; Signal.  
 FT SIGNAL 1 17 Potential.  
 FT CHAIN 18 146 Interleukin-21.  
 FT DISULFID 64 115 /Ftrid=PRO\_0000015504.  
 FT DISULFID 71 118 Potential.  
 SQ SEQUENCE 146 AA; 16776 MW; PFE8DF836AF219AA CRC64;  
 Query Match 72.2%; Score 513; DB 1; Length 146;  
 Best Local Similarity 80.6%; Pred. No. 2.9e-39;  
 Matches 100; Conservative 7; Mismatches 17; Indels 0; Gaps 0

QY 2 QGODRHHIRKRLIDIVDQKKNVNDLVPEPLPAPEDVETNCWSSAFSCFOKAOLKANT 61  
 Db 23 QEDQLLIRKRLIDIVDQKKNVNDLVPEPLPAPEDVETNCWSSAFSCFOKAOLKANT 82

QY 62 GNNERRIIVSISKLKRKPPSTNAGRGKRLTCPCSDCYEKKPKPEFLERFKSLQKMIH 121  
 Db 83 GANNQIINVLTKQKRLPPTNAGRGKRPACPCSDCYEKAPKEFLERFKSLQKMIH 142

QY 122 QHLS 125  
 Db 143 QHLS 146

RESULT 5  
 IL21\_MOUSE  
 ID IL21\_MOUSE STANDARD; PRT; 146 AA.  
 AC Q9BS17;  
 DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAR-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 24.  
 DN Interleukin-21 precursor (IL-21).  
 GN Name=IL21;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RN NCBIOTIDE SEQUENCE [mRNA].  
 RC STRAIN=BALB/c;  
 RX MEDLINE=20531754; PubMed=11081504; DOI=10.1038/35040504;  
 RA Parrish-Bovek J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,  
 RA Grosse J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,  
 RA Burkhead S., Heipel M., Brandt C., Kuilper J.L., Kramler J.,

RA Conklin D., Preenell S.R., Berry J., Shiota F., Bort S., Hamblly K.,  
RA Mndri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,  
RA Raymond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,  
RA Maurer M., Kaushansky K., Holly R.D., Foster D.,  
RT "Interleukin 21 and its receptor are involved in NK cell expansion and  
RT regulation of lymphocyte function.";  
RN Nature 408:57-63(2000).  
RP NUCLEOTIDE SEQUENCE [mRNA].  
RC STRAIN=BALB/c;  
RA Guobing C., Jun D., Junsong C., Fenhui Z.;  
RT "Mouse interleukin 21 can improve the anti-tumor effect of LAK  
RT cells.";  
RN Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
RX FUNCTION, AND SUBCELLULAR LOCATION.  
RX PubMed=11970879; DOI=10.1016/S1074-7613(02)00295-9;  
RA Kasalan M.T., Whitters M.J., Carter L.L., Lowe L.D., Jusaf J.M.,  
RA Deng B., Johnson K.A., Wittek J.S., Senices M., Konz R.F.,  
RA Wurster A.L., Donaldson D.D., Collins M., Young D.A., Grusby M.J.;  
RT "IL-21 limits NK cell responses and promotes antigen-specific T cell  
RT activation: a mediator of the transition from innate to adaptive  
RT immunity";  
RN Immunity 16:559-569(2002).  
RA [4]  
RN FUNCTION.  
RX PubMed=12893770; DOI=10.1182/blood-2003-03-0669;  
RA Brandt K., Bulfone-Paus S., Foster D.C., Rueckert R.;  
RT "Interleukin-21 inhibits dendritic cell activation and maturation.";  
RN Blood 102:4090-4098(2003).  
RP [5]  
RN FUNCTION.  
RX PubMed=15100251;  
RA Pene J., Gauchat J.F., Lecart S., Drouet E., Guglielmi P., Boulay V.,  
RA Delwail A., Foster D., Lecron J.C., Yssel H.;  
RT "IL-21 is a switch factor for the production of IgG1 and IgG3 by human  
RT B cells.";  
RN Immunol. 172:5154-5157(2004).  
CC -I- FUNCTION: Cytokine with immunoregulatory activity. May promote the  
CC transition between innate and adaptive immunity. Induces the  
CC production of IgG(1) and IgG(3) in B-cells. May play a role in  
CC proliferation and maturation of natural killer (NK) cells in  
CC synergy with IL15. May regulate proliferation of mature B- and T-  
CC cells in response to activating stimuli. In synergy with IL15 and  
CC IL18 stimulates interferon gamma production in T-cells and NK  
CC cells (by similarity). During T-cell mediated immune response may  
CC inhibit dendritic cells (DC) activation and maturation.  
CC -I- SUBCELLULAR LOCATION: Secreted protein.  
CC -I- SIMILARITY: Belongs to the IL-21 family.  
CC  
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CC  
CC EMBL: AF254070; AAC29349.1; -; mRNA.  
CC EMBL: AY428162; AAR06254.1; -; mRNA.  
CC Ensemble1; ENSMUSG0000027718; Mus musculus.  
CC MGI: MGI.1890474; Il21.  
CC GO: GO:0005615; C:extracellular space; TAS.  
CC GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .); IDA.  
CC GO: GO:0045579; P:positive regulation of B cell differentiation; NAS.  
CC GO: GO:0001783; P:programmed cell death, B cells; NAS.  
CC Cytokine; Glycoprotein; Signal.  
CC SIGNAL 1 17 Potential.  
CC CHAIN 18 146 Interleukin-21.  
CC FT CARBOHYD 85 85 /FTid=PRO\_0000015506.  
CC FT DISULFID 64 115 N-linked (GlcNAc. . .) (Potential).  
CC FT DISULFID 71 118 Potential.  
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;  
Query Match 56.8%; Score 404; DB 1; Length 146;  
Best Local Similarity 62.1%; Pred. No. 3.3e-29;  
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 2 QGODRHIMRKQLIDIVDQKNYVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANT 61  
DB 23 QGPRLLIRLRHLIDIVEQKTYENDLPPELLSAPQGVKGCHHAAPACFOKAKLKSNP 82  
QY 62 GNNERTIIVNSIKKLKRRKPSTNAGRRQKRLTCPSCDSEYKKPKFLEPKSLIQMII 121  
DB 83 GNNKTFIIDVAQLRRLPARGGKKQKHAKCPSCDSEYKRTPKFLEPKSLIQMII 142  
QY 122 QHLS 125  
DB 143 QHLS 146  
RESULT 6  
ID QSEUE2\_MOUSE PRELIMINARY; PRT; 146 AA.  
AC QSEUE2;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DE 07-FEB-2006, entry version 3.  
DE Interleukin 21.  
GN Name=Il21; ORFNames=DN-452A22.7-001;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Pandian R.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
CC  
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CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC  
CC EMBL: AL645982; CA126234.1; -; Genomic DNA.  
CC Ensemble1; ENSMUSG0000027718; Mus musculus.  
SQ SEQUENCE 146 AA; 16811 MW; D2527ED95BA15194 CRC64;  
Query Match 56.8%; Score 404; DB 2; Length 146;  
Best Local Similarity 62.1%; Pred. No. 3.3e-29;  
Matches 77; Conservative 19; Mismatches 28; Indels 0; Gaps 0;  
QY 2 QGODRHIMRKQLIDIVDQKNYVNDLVPEFLPAPEDVETNCESAFSCFOKAQLKSANT 61  
DB 23 QGPRLLIRLRHLIDIVEQKTYENDLPPELLSAPQGVKGCHHAAPACFOKAKLKSNP 82  
QY 62 GNNERTIIVNSIKKLKRRKPSTNAGRRQKRLTCPSCDSEYKKPKFLEPKSLIQMII 121  
DB 83 GNNKTFIIDVAQLRRLPARGGKKQKHAKCPSCDSEYKRTPKFLEPKSLIQMII 142  
QY 122 QHLS 125  
DB 143 QHLS 146  
RESULT 7  
ID IL21\_PERMA STANDARD; PRT; 123 AA.  
AC Q80XG2;  
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.  
DT 01-JUN-2003, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE Interleukin-21 precursor (IL-21) (Fragment).  
GN Name=Il21;  
OS Peromyscus maniculatus (Deer mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridea; Cricetidae; Neotominae; Peromyscus.  
OX NCBI\_TaxId=10042;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [mRNA].



RA Schountz T., Buniger A., Davenport B., Hegg T.,  
 RT "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4  
 RL CDNA's";  
 CC Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cycokine with immunoregulatory activity. May promote the  
 CC transition between innate and adaptive immunity. Induces the  
 CC production of IgG(1) and IgG(3) in B-cells. May play a role in  
 CC proliferation and maturation of natural killer (NK) cells in  
 CC synergy with IL15. May regulate proliferation of mature B- and T-  
 CC cells in response to activating stimuli. In synergy with IL15 and  
 CC IL18 stimulates interferon gamma production in T-cells and NK  
 CC cells (By similarity). During T-cell mediated immune response may  
 CC inhibit dendritic cells (DC) activation and maturation (By  
 CC similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the IL-21 family.  
 CC -----  
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 CC -----  
 DR EMBL; AY247761; AAP04420.1; -; mRNA.  
 KM Cycokine; Glycoprotein; Signal.  
 FT SIGNAL 1 10 Potential.  
 FT CHAIN 11 123 Interleukin-21.  
 FT CARBOHYD 77 77 /FTid=PRO\_0000015507.  
 FT DISULFID 56 107 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 63 110 Potential.  
 FT NON\_TER 1 1 Potential.  
 FT NON\_TER 123 123 Potential.  
 SQ SEQUENCE 123 AA; 13945 MW; 8656C8EA95447E34 CRC64;  
 Qy Query March 48.4%; Score 344; DB 1; Length 123;  
 Db Best Local Similarity 59.6%; Pred. No. 9.2e-24; Indels 0; Gaps 0;  
 Matches 65; Conservative 21; Mismatches 23;  
 Qy 2 QGQDRHMRIMRQQLDIYDQKNYVNDLVEFLPAPEDEVETNCESAFSCFQKAKLSANT 61  
 Db 15 QRPRLRLRLHLDVNDVQGLKIVYDDLPBLLPAQDVKHBHSAFQCFQAKLKPANT 74  
 62 GNNERIIVNSIKKLKRKPPSTNAGRRQKRLTCPSGDSYEKKPPEFLE 110  
 75 GSNKTIISDLVTQLRRRLPATKAEKKQSLVCPSCDSYEKKTPPEFLE 123  
 Db  
 RESULT 8  
 ID Q58IU6\_CHICK PRELIMINARY; PRT; 145 AA.  
 AC Q58IU6;  
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
 DT 26-APR-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 4.  
 OS Gallus gallus (Chicken).  
 DE Interleukin 21.  
 CC Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Shao J., Dong W., Xiang L.;  
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 DR EMBL; AY943833; AAX40651.1; -; mRNA.  
 KM SEQUENCE 145 AA; 16637 MW; E70AB6A568CDABE6 CRC64;  
 Qy Query March 21.0%; Score 149.5; DB 2; Length 145;  
 Db Best Local Similarity 32.0%; Pred. No. 9.4e-06;  
 Matches 39; Conservative 20; Mismatches 52; Indels 11; Gaps 4;

Qy 9 IRMRQLIDIVDQKNYVNDLVEFLPAPEDEVETNCESAFSCFQKAKLSANTGNNERI 68  
 Db 26 MKRYQSKTIDHLDKVDVQKVEELHTPEBPGDGLTAIVTCFQNGILKLPKNSQVNAV 85  
 Qy 69 NVSIKKLKRKP--PSTNAGRRQKRLTC--PSCDSYEKKPPEFLEFRFSLQKMTIHLS 125  
 Db 86 FAKTVKTIIRRLPPLVPS-----EEH---CESCESEYERKKQPEFLNLSFKLQKLPKNSSTA 137  
 Qy 126 SR 127  
 Db 138 ER 139  
 RESULT 9  
 ID IL15\_FELCA STANDARD; PRT; 162 AA.  
 AC O97687;  
 DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.  
 DT 01-MAY-1999, sequence version 1.  
 DT 07-FEB-2006, entry version 23.  
 DE Interleukin-15 precursor (IL-15).  
 GN Name=IL15;  
 OS Felis silvestris catus (Cat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;  
 CC Felinae; Felis.  
 OC NCBI\_TaxID=9685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [mRNA].  
 RC TISSUE=Lymph node;  
 RA Barger A.B., Dean G.A., Lavoie A.S.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Cycokine that stimulates the proliferation of T-  
 CC lymphocytes. Stimulation by IL-15 requires interaction of IL-2R  
 CC with components of IL-2R, including IL-2R beta and probably IL-2R  
 CC gamma but not IL-2R alpha (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted protein.  
 CC -1- SIMILARITY: Belongs to the IL-15 family.  
 CC -----  
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 CC -----  
 DR EMBL; AF108148; AAD05268.1; -; mRNA.  
 DR InterPro; IPR003443; Interleukin\_15.  
 DR PANTHER; PTHR11323; Interleukin\_15; 1.  
 DR Pfam; PF02372; IL15; 1.  
 KM Cycokine; Glycoprotein; Signal.  
 FT SIGNAL 1 29 Potential.  
 FT PROPEP 30 48 Potential.  
 FT CHAIN 49 162 /FTid=PRO\_0000015395.  
 FT CARBOHYD 104 104 Interleukin-15.  
 FT CARBOHYD 127 127 /FTid=PRO\_0000015396.  
 FT DISULFID 83 133 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 90 136 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 162 AA; 18412 MW; D8C7CEFF740110DD CRC64;  
 Qy Query March 14.3%; Score 101.5; DB 1; Length 162;  
 Db Best Local Similarity 26.5%; Pred. No. 0.28;  
 Matches 31; Conservative 19; Mismatches 48; Indels 19; Gaps 5;  
 Qy 16 DIVDQLK---NYVNDL--VPEFLPAPEDEVETNCESAFSCF-----QKAKLSANTGNNERI 67  
 Db 52 DVIDLKLIDKTIOSLHLDATLYESDVHPCKVYAMKCFLELHVLVSLESKNETIHQTV 111  
 Qy 68 INVSIIKKLKRKPPSTNAGRRQKRLTC--PSCDSYEKKPPEFLEFRFSLQKMTIHLS 121  
 Db 112 ENII-----LANSGLSENRIITETGCKECELEKNIKKEFLQSPVHIVQPFIN 160  
 RESULT 10  
 Qy Q6FGX7\_HUMAN

ID O6FGK7\_HUMAN PRELIMINARY; PRT; 135 AA.  
 AC O6FGK7;  
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DE IL15 protein (Interleukin 15, isoform 2).  
 GN Name=IL15;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hallack A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,  
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
 RA Korn B., Zuo D., Hu Y., Labaer J.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M., Uedin T.B., Topolycki S., Canninci P., Prange C.,  
 RA Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RL "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RG NIH MGC Project;  
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Li C.;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
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 CC -----  
 DR EMBL: BC100962; AAI00963.1; -; mRNA.  
 DR EMBL: CR542007; CAG46804.1; -; mRNA.  
 DR EMBL: AY720442; AAU21241.1; -; mRNA.  
 DR EMBL: CR541980; CAG46777.1; -; mRNA.  
 DR EMBL: BC100961; AAI00962.1; -; mRNA.  
 DR Ensembl: ENSG00000164136; Homo sapiens.  
 DR GO: GO:0005576; C:extracellular region; IEA.  
 DR GO: GO:0005126; F:hematopoietic/interferon-class (D200-domain. .; IEA.  
 DR GO: GO:0006955; P:immune response; IEA.  
 DR InterPro: IPR003443; Interleukin\_15.  
 DR PANTHER: PTHR11323; Interleukin\_15; 1.  
 DR Pfam: Pf02372; IL15; 1.  
 SQ SEQUENCE 135 AA; 14912 MW; EB4F422096B143B CRC64;

QY 15 IDIVDLKNTVNDLVPEF-----LPAPDYETNCENASFSGF-----QKALQKANTGNNE 65  
 Db 24 VNVISDLKK-IEBILQSHMIDATLYTESDVHPSCKVTAMCFLLLELOVISIESGDAS1HD 82  
 QY 66 RIINVSIKLKKRPSPNAGRROKRLTSCPSCSYEKKPPKFLERKSLQKKI 121  
 Db 83 TWENTLI--LANNLSLSNGVNTES--GCKECELSEKNIKEFLLQSFVHIVQMFIN 133  
 RESULT 11  
 IL15\_HUMAN STANDARD; PRT; 162 AA.  
 AC P40933; O00440; O43512; Q93058; Q9UBA3; Q9UBA3; Swiss-Prot.  
 DT 01-FEB-1995, integrated into UniProtKB/Swiss-Prot.  
 DT 01-FEB-1995, sequence version 1.  
 DE 07-FEB-2006, entry version 43.  
 DE Interleukin-15 precursor (IL-15).  
 GN Name=IL15;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=94233380; PubMed=8178155;  
 RA Grabstein K.H., Eisenman J., Shanebeck K., Rauch C., Srinivasan S.,  
 RA Pung V., Beers C., Richardson J., Schoenborn M.A., Abdieh M.,  
 RA Johnson L., Alderson M.R., Watson J.D., Anderson D.M., Gird J.G.;  
 RT "Cloning of a T cell growth factor that interacts with the beta chain  
 RT of the interleukin-2 receptor";  
 RL Science 264:965-968(1994).  
 [2]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S48AA).  
 RA Krause H., Jandrig B., Wernicke C., Bulfone-Paus S., Pohl T.,  
 RA Diamantstein T.;  
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).  
 RC TISSUE=Lung cancer;  
 RX MEDLINE=96218668; PubMed=8668345.  
 RA Meazza R., Verdiani S., Biassoni R., Coppolecchia M., Gaggero A.,  
 RA Orenzo A.M., Colombo M.P., Azzone B., Ferrini S.;  
 RT "Identification of a novel interleukin-15 (IL-15) transcript isoform  
 RT generated by alternative splicing in human small cell lung cancer cell  
 RT lines";  
 RL Oncogene 12:2187-2192(1996).  
 [4]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM IL15-S21AA).  
 RC TISSUE=Testis;  
 RX MEDLINE=98070771; PubMed=9405632; DOI=10.1073/pnas.94.26.14444;  
 RA Tgaya Y., Kury S., Thies T.A., Losi J.M., Azimi N., Hanover J.A.,  
 RA Barford R.N., Waldmann T.A.;  
 RT "Generation of secretable and nonsecretable interleukin 15 isoforms  
 RT through alternate usage of signal peptides";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:14444-14449(1997).  
 [5]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 3).  
 RA Meazza R., Ferrini S.;  
 RT "Expression of two IL-15 mRNA isoforms in human tumors does not  
 RT correlate with secretion: role of different signal peptides";  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 [6]  
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA) (ISOFORM IL15-S48AA).  
 RC TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP NUCLEOTIDE SEQUENCE OF 49-162.  
 RC TISSUE=Epidermis.  
 RA Sorel M.A., Jacques Y.,  
 RT "IL15 expression in human keratinocytes";  
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.  
 CC -1 FUNCTION: Cytokine that stimulates the proliferation of T-  
 CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15  
 CC with components of IL-2R, including IL-2R beta and probably IL-2R  
 CC gamma but not IL-2R alpha.  
 CC -1 SUBCELLULAR LOCATION: Secreted (IL15-S48AA). IL15-S21AA is not  
 CC secreted, but rather is stored intracellularly, appearing in the  
 CC nucleus and cytoplasmic components.  
 CC -1 ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=IL15-S48AA;  
 CC IsoId=P40933-1; Sequence=Displayed;  
 CC Name=IL15-S21AA;  
 CC IsoId=P40933-2; Sequence=VSP\_002660;  
 CC Name=3;  
 CC IsoId=P40933-3; Sequence=VSP\_002661;  
 CC -1 TISSUE SPECIFICITY: Most abundant in placenta and skeletal muscle.  
 CC It is also detected in the heart, lung, liver and kidney. IL15-  
 CC S21AA is preferentially expressed in tissues such as testis and  
 CC thymus.  
 CC -1 SIMILARITY: Belongs to the IL-15 family.  
 CC -1 DATABASE: NMBE=K&D Systems' cytokine source book: IL15;  
 CC WWW="http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyId=209".  
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 CC -----  
 CC EMBL: U14407; AAA21551.1; -; mRNA.  
 CC EMBL: X91233; CA62616.1; -; Genomic DNA.  
 CC EMBL: X94223; CA63914.1; -; mRNA.  
 CC EMBL: X94222; CA63913.1; -; mRNA.  
 CC EMBL: AF031167; AAB87518.1; -; mRNA.  
 CC EMBL: Y09908; CA471044.1; -; mRNA.  
 CC EMBL: BC018149; AAH18149.1; -; mRNA.  
 CC EMBL: Z38000; CA86100.1; -; mRNA.  
 CC Ensembl: ENSG00000164136; Homo sapiens.  
 DR HGNC: HGNC:5977. IL15.  
 DR MTM; 600554; gene.  
 DR GO: GO:0005768; C:endosome; TAS.  
 DR GO: GO:0005615; C:extracellular space; TAS.  
 DR GO: GO:0005794; C:Golgi apparatus; TAS.  
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO: GO:0005624; C:membrane fraction; TAS.  
 DR GO: GO:0004871; P:signal transducer activity; TAS.  
 DR GO: GO:0007267; P:cell-cell signaling; TAS.  
 DR GO: GO:0006955; P:immune response; TAS.  
 DR GO: GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR GO: GO:0007165; P:signal transduction; TAS.  
 DR InterPro: IPR003443; Interleukin\_15.  
 DR PANTHER: PTHR11323; Interleukin\_15; 1.  
 DR Pfam: Pf02372; IL15; 1.  
 KW Alternative splicing; Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 29 Potential.  
 FT PROPEP 30 48 Potential.

FT FT CHAIN 49 162 /FTid=PRO\_0000015393.  
 FT FT Interleukin-15.  
 FT FT CARBOHYD 127 127 /FTid=PRO\_0000015394.  
 FT FT DISULFID 83 133 N-linked (GlcNAc...) (Potential).  
 FT FT DISULFID 90 136 Potential.  
 FT FT VASAPLIC 1 47 Potential.  
 FT FT MRISKPHRSISICQCYCLINSHFLTAGIHVPIIGCSA  
 FT FT GLPKTE -> MDPVOIIFSFLISASVIMSR (in  
 FT FT isoform 3).  
 FT FT VASAPLIC 1 37 /FTid=VSP\_002661.  
 FT FT MRISKPHRSISICQCYCLINSHFLTAGIHVPIIG ->  
 FT FT VLVGTIDCS (in isoform IL15-S21AA).  
 FT FT /FTid=VSP\_002660.  
 FT FT E -> K (in Ref. 4).  
 SQ SEQUENCE 162 AA; 18086 MW; 0CE0520C1D8379E2 CRC64;  
 Query Match 14.0%; Score 99.5; DB 1; Length 162;  
 Best Local Similarity 25.9%; Pred. No. 0.43; Indels 15; Gaps 5;  
 Matches 30; Conservative 23; Mismatches 48;  
 Qy 15 IDIYDQKNVNDIVPEF-----LPAPDEVTCNCSAFSCF-----QKQKLSANTGNN 65  
 Db 51 VNVISDLKK-IEDLIQSMHIDATYTESDVHPCKVTAMKCFLELYVISLESQDASIH 109  
 Qy 66 RINWSIKKLRKPPSTNAGRQRHRLTCSQDSYEKKPPKFLERFKSLLOQKIH 121  
 Db 110 TVEHLIT-LANNLSNGNTES---GCKECEELEKNIEKPIQSFVHIQWFIN 160  
 RESULT 12  
 Q99528 HUMAN  
 ID Q99528 HUMAN PRELIMINARY; PRT; 162 AA.  
 AC Q99528  
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.  
 DT 13-SEP-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 2.  
 DR Interleukin 15, isoform 1.  
 GN Name:IL15;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=PCR rescued clones;  
 RG NIH WGC Project;  
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.  
 CC -----

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DR EMBL: BC100963; AA100964.1; -; mRNA.  
DR GO: GO:0005576; C:extracellular region; IEA.  
DR GO: GO:0005126; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO: GO:0006955; P:immune response; IEA.  
SQ SEQUENCE 162 AA; 18086 MW; 0CE0520CD8379E2 CRC64;  
  
Query Match 14.0%; Score 99.5; DB 2; Length 162;  
Best Local Similarity 25.9%; Pred. No. 0.43;  
Matches 30; Conservative 22; Mismatches 48; Indels 15; Gaps 5;  
  
QY 15 IDIVDQKNYNDVLPF-----LPAPDEVTCNCSAFSCF-----QKAOLKSANTGNNE 65  
DB 51 VNVISDIKK-IEDLIQSMHIDATLYTESDHPSCVKYAMKCFLELQVLSIESGDASIH 109  
QY 66 RIINVSIKLKRKPPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQKMH 121  
DB 110 TVENLII--LANNSLSSNGVTS--GCKECELKEKNITFLOSFIHIVQMFIN 160  
  
RESULT 13  
IL15\_RABIT STANDARD; PRT; 162 AA.  
AC Q3Y568;  
DT 06-DEC-2005, integrated into UniProtKB/Swiss-Prot.  
DT 27-SEP-2005, sequence version 1.  
DT 07-MAR-2006, entry version 6.  
DE Interleukin-15 precursor (IL-15).  
GN Name=IL15;  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;  
OC Oryctolagus.  
OX NCBI\_TaxID=9986;  
[1]  
Nucleotide Sequence [mRNA], AND TISSUE SPECIFICITY.  
RX PubMed=15978671; DOI=10.1016/j.yetimm.2005.04.013;  
RA Xiong C., Hixson P.M., Mendoza L.H., Smith C.W.;  
RT "Cloning and expression of rabbit interleukin-15."  
RL Vet. Immunol. Immunopathol. 107:131-141(2005).  
CC -!- FUNCTION: Cytokine that stimulates the proliferation of T-  
CC lymphocytes. Stimulation by IL-15 requires interaction of IL-15  
CC with components of IL-2R, including IL-2R beta and probably IL-2R  
CC gamma but not IL-2R alpha (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted protein.  
CC -!- TISSUE SPECIFICITY: Expressed in many tissues including heart,  
CC spleen, lung, liver, muscle and kidney (at mRNA level). Expressed  
CC in many tissues including heart, spleen, lung, liver, muscle and  
CC kidney (at protein level).  
CC -!- SIMILARITY: Belongs to the IL-15 family.  
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-----  
DR EMBL: DQ157452; AA282803.1; -; mRNA.  
DR InterPro: IPR003443; Interleukin\_15.  
DR PANTHER: PTHR11323; Interleukin\_15; 1.  
DR Pfam: PF02372; IL15; 1.  
KW Cytokine; Glycoprotein; Signal.  
FT SIGNAL 1 29 potential.  
FT PROPEP 30 48 potential.  
FT CHAIN 49 162 /FTID=PRO\_0000043393.  
FT FTID=PRO\_0000043394.  
FT CARBOHYD 108 108 /FTID=PRO\_0000043394. (Potential).  
FT CARBOHYD 119 119 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 127 127 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 143 143 N-linked (GlcNAc. . .) (Potential).  
FT DISULFID 83 133 N-linked (GlcNAc. . .) (Potential).  
FT DISULFID 90 136 potential.  
SQ SEQUENCE 162 AA; 18330 MW; 6F9C7C129FB64B9 CRC64;

Query Match 13.9%; Score 98.5; DB 1; Length 162;  
Best Local Similarity 27.1%; Pred. No. 0.54;  
Matches 32; Conservative 17; Mismatches 48; Indels 21; Gaps 5;  
  
QY 16 DIVDQKNYNDVLPF-----LPAPDEVTCNCSAFSCF-----QKAOLKSANTGNNE 66  
DB 52 DIVSDLR-IEDLIKSIHIDATLYTESDHPNCKVYAMKCFLELRVISHESRMNDINET 110  
QY 67 RIINVSII--KKLKRKPPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQKMH 121  
DB 111 VQNLIIANSLSSKNGVTSG-----CKECELKEKNITFLOSFIHIVQMFIN 160  
  
RESULT 14  
ID 05W7F5 BRARE PRELIMINARY; PRT; 162 AA.  
AC 05W7F5;  
DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.  
DT 07-DEC-2004, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Interleukin-15 1.  
GN Name=im:7142994; Synonyms=IL-15 1;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hama S., Ram S., Sakai M.;  
RT "Cloning of interleukin 15 genes from zebrafish."  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
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DR EMBL: AB194244; BAD69558.1; -; mRNA.  
DR Ensembl: ENSDARG0000007743; Danio rerio.  
DR ZFIN: ZDB-GENE-041111-173; Im:7142994.  
SQ SEQUENCE 162 AA; 18924 MW; F0C9F389C7A392DE CRC64;  
  
Query Match 13.6%; Score 96.5; DB 2; Length 162;  
Best Local Similarity 24.2%; Pred. No. 0.82;  
Matches 29; Conservative 26; Mismatches 40; Indels 25; Gaps 5;  
  
QY 12 RQIIDIYDQ-----IKNYNDVLPFELPAPDEVTCNCSAFSCQ-----KAOLKSA 59  
DB 48 RESVEWYKQIAAKLNNVNDQM--MYTPTQMYK-NCSSKSTTTCFAFVSVLSEIVQEST 105  
QY 60 NTGNNRIINVSIIKLRKPPSTNAGRQKRLTCPSCDSEYKKPKPEFLERFKSLQKMH 119  
DB 106 AFRQLRIILNRVYKRL-----QDEMCKKPCVCELYKBSYTFPLNTIQLHLEQM 154  
  
RESULT 15  
Q32PM5 BRARE PRELIMINARY; PRT; 160 AA.  
AC Q32PM5;  
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 3.  
DE Zgc:123044.  
GN ORFNames=zgc:123044;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Search completed: August 14, 2006, 21:51:42  
Job time : 304 secs

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